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  Sequence 2, A Sequence 3, A Sequence 25, A Sequence 25, Sequence 1, A Sequence 11, A Sequence 11, A Sequence 7, A Sequence 1, A 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Collmer, Alan
APPLICANT: Charkowski, Amy
APPLICANT: Charkowski, Amy
APPLICANT: Alano, James R.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELLCITOR FROM
TITLE OF INVENTION: PSEUDOMONAS SYRINGAE AND ITS USE
ONR
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 155.2; DB 4;
Pred. No. 1e-38;
0; Mismatches 233;
US-08-530-797-2
US-08-298-819-3
US-08-185-970A-25
US-07-885-970A-25
US-08-288-687A-25
US-08-185-233A-1
US-08-185-233A-1
US-09-041-886-18
US-09-179-558-62
US-09-179-558-62
US-08-173-508-7
US-08-173-508-7
US-08-173-508-7
US-08-265-310-7
US-08-385-74-9
US-08-388-574-9
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REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1741
TELECOMMUNICATION INFORMATION:
TELEPAN: (716) 263-1304
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,107
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09120817
Patent No. 6172184
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 57.1%;
Matches 330; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE:
US-09-120-817-1
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    Search time 43.71 Seconds (without alignments) 5820.960 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-402-668-9
US-08-232-463-14
US-08-233-4438-1
US-08-961-083-187
US-08-658-136-2
US-08-658-136-1
US-08-658-136-1
US-08-658-136-1
US-08-945-848-7
US-08-945-848-7
US-08-945-848-6
US-09-9430-114-2
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S-08-403-852D-6
S-08-510-646B-6
S-09-231-818-6
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                                                                                                                                     October 21, 2001, 10:47:22
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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                                      1079 GCCGCCAAGATCAATGTGGTGAAAGACACCCATCAAGGTCGGCGCTGGCGAAGTCTTTGAC 1138
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                                                                                ggcaaaggacaaaccttcaccgccggttcagaattaggcgatggcggccagtctgaaaac 864
  ggcgctaatcagacggtgctgcatgacaccattaccgtgaaaggcgggtcaggtgtttgat
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CURRENT APPLICATION NUMBER: US/09/402,668
CURRENT APPLICATION NUMBER: 1998-10-08
PRIOR APPLICATION NUMBER: 9-091142 JAPAN
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1998-010
PRIOR FILING DATE: 1998-010
SOFTWARE: PALENT NOS: 14
SOFTWARE: PALENT NOS: 14
SOFTWARE: PALENT NOS: 14
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Patent No. 6172030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WADA, Yasunao
APPLICANT: KASAI, Miyuki
APPLICANT: SHIKATA, Shitsuw
APPLICANT: SUZUMATSU, Atsushi
APPLICANT: KOIKE, Kenzo
APPLICANT: HATADA, Yuji
APPLICANT: TOO, Susumu
APPLICANT: TOO, Susumu
APPLICANT: TSUMADORI, Masaki
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ORGANISM: Bacillus sp.
FEATURE:
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US-09-402-668-1
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APPLICANT: Anderson, Lene N.
APPLICANT: Schulein, Martin
APPLICANT: Scholein, Martin
APPLICANT: Lange, Niels Erik K.
APPLICANT: Lange, Niels Erik K.
APPLICANT: Schnorr, Kirk
TITLE OF INVENTION: Pectaniformis
TITLE OF INVENTION: Licheniformis
FILE REFERENCE: 5377.200-US
CURRENT APPLICATION NUMBER: US/09/198,956
CURRENT APPLICATION NUMBER: 1144/97
EARLIER APPLICATION NUMBER: 1997-11-24
EARLIER PELING DATE: 1997-11-24
EARLIER PELING DATE: 1997-11-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FASTEEQ for Windows Version 3.0
                                                                                                                         Length 591;
                                                                                                                           Score 94.8; DB 4; Length 5 Pred. No. 4.8e-20; 0; Mismatches 217; Indels
CTHER INFORMATION: Strain: KSM-P15; NAME/KEY: CDS; LOCATION: (1)..(591)
US-09-402-668-1
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; Patent No. 6165769
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US-09-198-956-3
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                       874 ctgtttatactggaagacggtgccagcctgaaaaacgtcaccatgggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                606 aacgtcccctacctcaccgcttgatttcccttcttctcccacc 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                        Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATORNEY/AGENT INFORMATION:
NAME: BENY. Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                       Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135;
                                                                                                                                                                                                                                                                                           SSEE: Foley & Lardner r: 1800 Diagonal Road, Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.48;
4.98; P
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703)683-4109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                        TITLE OF INVENTION: RENUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                           RESULT 5
US-08-232-463-14
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                                                                                                                                                                                        tattcatctttacggtgatgccaaaatagacaatctgcacgtcaccaacgtgggtgagga 998
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                   Length 666;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                   0; Mismatches 113; Indels
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63.3%; Pred. No. 5.3e-09;
                 Score 74.2; DB 4;
Pred. No. 1.5e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 2173-0116P
CURRENT APPLICATION NUMBER: US/09/402,668
CURRENT FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 9-091142 JAPAN
PRIOR PELING DATE: 1997-04-09
PRIOR FILING DATE: 1997-04-09
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1997-09-08
PRIOR FILING DATE: 1998-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09402668
Patent No. 6172030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WADA, Yasunao
KASAI, Miyuki
SHIKATA, Shitsuw
SUZUWATSU, Atsushi
KOIKE, Kenzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                 5.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KOIKE, Kenzo
APPLICANT: HATADA, Yuji
APPLICANT: KOBAYASHI, Tohru
APPLICANT: ITO, Susuum
APPLICANT: TSUWADORI, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Ver. 2.1
             Query Match
Best Local Similarity 55.73
Matches 142; Conservative
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APPLICANT:
APPLICANT:
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FILING DATE: 18 CLASSIFICATION:
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TOPOLOGY: 1in
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                                                                                                                                                        418 gc 419
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 gggggggacaacgggcttggtggtcataatgcaaattctgcgttggggcaacaacccatc 117
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SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FILTE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43.2; DB Pred. No. 0.0036;
                                                                                                                                                                                                                                                    ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: NA
COUNTRY: USA
LIP: 22313-0299
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                              Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.2%; So
Best Local Similarity 5.8%; Pre
Matches 21; Conservative 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29,768
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TYPE: nucleic acid
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                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF TITLE OF INVENTION: CUROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL TITLE OF INVENTION: TRANSLATIONS ASSOCIATED NITH THE DESCREPCIONENT OF CANCEROUS TITLE OF INVENTION: TRANSLOCATIONS AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
                                  298 agtcagaacatgctgagtgagatgggcaacaacgggctggatcaggccatcacgcccgat 357
                                                                                                      358 ggccagggcggcggatcggcgataatcctttactgaaagccatgctgaagcttatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: ABDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
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APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Melot, Thomas
APPLICANT: Peter, Martine
APPLICANT: Phomogastel, Beatrice
APPLICANT: Thomas, Gilles
APPLICANT: Zucman, Jessica
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08343443B Patent No. 5968734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delattre, Olivier
Desmaze, Chantal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1
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nucleic acid
EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                             1969 GACGGTGCTCGCCTTTATCCATTTTTCCAGGTCCTCCACGTCCTCTTCTTCTTCCTCCA 1910
                                                                                      534 gaaggccccttccggcaactccccttccggcaactactctcccgtcagtaccttctcacc 593
                                                                                                                                                                      594 cccatccacgccaacgtcccctacctcacgcttgatttcccttctccccaccaaagc 653
                                                                                                                                                                                                                                                    654 agccggggggaggaacgccggtaaccgatcatcctgaccctgttggtagcgcggggatcgg 713
                                               Gaps
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Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Chol et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      714 ggccggaaattcggtggccttcaccagcgccggcgctaatcagacggtgctgcatgacac
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  Length 2371;
Score 37.4; DB 2; Length 2 Pred. No. 0.12; 0; Mismatches 131; Indels
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COMPUTER READABLE FORM:
MEDIUM TREADABLE FORM:
COMPUTER: HP Vectra 486/33
COMPUTER: HP Vectra 486/33
SOFTWARE: ASOLI Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Brookes, A. Anders
REGISTRATION UNDBER: 36,373
REPERENCE/DOCKET NUMBER: PB34C
TELECOMMUNICATION INPORMATION:
TELEFAX: (301) 309-8514
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
    Query Match
Best Local Similarity 47.0%;
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 400 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-961-083-187
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aaatggeteaattattggeggaactgttaaagteactgetategeeacaateaggtaatg 196
                                     AAATCCAGCAATTAAGCACGGAATTGATCAAGGTTCTAGGACAGCTAGATGCAGAAAAAG 266
                                                                                 cggcaaccggagccggtggcaatgaccagactacaggagttggtaacgctggcggcctga
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                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPOUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35.8; DB 3;
Pred. No. 2.6;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEN4-17.8
                                                                                                                                                             257 acggacgaaaaggcacagcaggaac 281
                                                                                                                                                                                 ; Sequence 2, Application US/08658136 ; Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: ONE MOUNTAIN ROAD CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 53526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.7
Best Local Similarity 57.7
Matches 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MASSACHUSETTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE:
US-08-658-136-2
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                                                                                                                                                                                                                                                             RESULT 9
US-08-658-136-2
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STATE:
                                       207
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Gaps

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Indels

Query Match
2.7%; Score 36.2; DB 3;
Best Local Similarity 53.1%; Pred. No. 0.092;
Matches 77; Conservative 0; Mismatches 68;

Length 400;

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: Illinois
XY: United States of America
60606
                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
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US-08-945-848-7
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57.7%; Pred. No. 2.6;
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Patent No. 596872
GENERAL INFORMATION:
APPLICANT: MATSUSHIRO, ALZO
TITLE OF INVENTION: PEARL PROTEIN(NACREIN) AND PROCESS FOR TITLE OF INVENTION: THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Asrshain, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47; Indels
                                                                                                                                                                                                                          POLYCYSTIC KIDNEY DISEASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                    ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
                                                                                                                             APPLICANT: BURN, TIMOTHY C
APPLICANT: CONDORS, TIMOTHY D
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
TITLE OF INVENTION: POLYCYSTIC I
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSE: GENTYME CORPORATIO
                                                                                                                                                                                                                                                                                 E: GENZYME CORPORATION ONE MOUNTAIN ROAD
                                             Sequence 1, Application US/08658136 Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4
- TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEPHONE: 508-872-8415
                                                                                                KLINGER, KATHERINE
LANDES, GREGORY M
BURN, TIMOTHY C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 57.7
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
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                                                                                 GENERAL INFORMATION:
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US-08-945-848-7
                          US-08-658-136-1
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Patent No. 5968772

GENERAL INFORMATION:

APPLICANT: MATSUSHIRO, Aizo

TITLE OF INVENTION: PEARL PROTEIN(NACREIN) AND PROCESS FOR TITLE OF INVENTION: THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.2; DB 2; Length 1 Pred. No. 0.4; J. Mismatches 123; Indels
  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,848
                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Cawley, Jr, Thomas A.
REGISTRATION NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 19036/34324
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                      TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 7:
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Best Local Similarity 47.0%;
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1341 base pairs
TYPE: nucleic acid
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742..969
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724..727
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1123..1266
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21..51
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                       FILING DATE:
CLASSIFICATION: 435
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OPERATING SYSTEM:
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988 ccagetecteegteaceteeggeeceagetecteeateaceteeggeeceageteeteea 1047
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Sequence 10, Application PC/TUS9505741
GENERAL INFORMATION:
APPLICANT: Weintraub, Harold
APPLICANT: Lee, Jacqueline E.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Tapscott, Stephen J.
TITLE OF INVENTION: Neurogenic Differentiation (Neurob) Gene
TITLE OF INVENTION: and Protein
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1931;
                                                                                                                  APPLICANT: Horlick, Robert A.
APPLICANT: Bonaj, Bassam B.
APPLICANT: Robbins, Alan K.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes TITLE OF INVENTION: Erom Multiple Transfected Episomes FILE REFERENCE: 0867/J109030S1
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: EastSEQ for Mindows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34.6; DB 2; Length 1
Pred. No. 0.78;
0; Mismatches 109; Indels
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STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC.COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1048 teaceteeggeggeeceateteetgeact 1076
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                                                      ; Sequence 2, Application US/09130114; Patent No. 5976807; GENERAL INFORMATION:
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ATTORNEY AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 47.8 Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: EBNA
US-09-130-114-2
                                   JS-09-130-114-2
                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     857 ACAATGGGGACAACGGTAACAATGGAGACAACGGCAATAACGGCTACAATGGGGACAACG 916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 863 accagaaaccgctgtttatactggaagacggtgccagcctgaaaaacgtcaccatgggcg 922
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NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,848
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Pred. No. 0.57;
0; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cawley, Jr. Thomas A.
REGISTRATION NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 19036/34324
TELECOMMUNICATION INFORMATION:
TELEFAN: (312) 474-6300
TELEFAN: (312) 474-6300
TELEFAN: (312) 474-6300
SEQUENCE CHARACTERISTICS:
LENGTH: 2363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                       COUNTRY: United States of America 2IP: 60606
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Best Local Similarity 47.0%;
Matches 109; Conservative
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745..990
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1144..1287
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745..748
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CLASSIFICATION: 435
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                                                                                               CITY: Chicago
STATE: Illinois
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LOCATION:
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LOCATION:
FEATURE:
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LOCATION:
FEATURE:
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LOCATION:
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US-08-945-848-6
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Sequence 58, Application Sequence Address Sequence 
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN RC-BOS/MS-DOS
SOFTWARE: PATENTIN Rc-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
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NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REPERENCE/DOCKET NUMBER: 920043,403C2
FELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
TELEX: 3723836 SEDANBERRY
INFORMATION FOR SEO ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
                 FHCR-1-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FHCR TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100
TELEFAX: 206-225-0709
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
LENGTH: 485 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: 1481
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Best Local Similarity 62.1
Matches 54; Conservative
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STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
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LOCATION:
PCT-US95-05741-10
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                                                                                                                       Length 456;
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                                                                                                                      Score 34; DB 1;
Pred. No. 0.49;
0; Mismatches 55
                                                                                                                    2.5%;
ilarity 54.9%;
Conservative C
TYPE: nucleic acid
                         TOPOLOGY: linear FEATURE:
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Best Local Similarity
Matches 67; Conserv
                                                   ; NAME/KEY: CDS
; LOCATION: 1..4
US-08-233-788A-58
            STRANDEDNESS:
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Human Ews gene (ge
HSV-2 strain SB5 C
Corynebacterium gl
Streptococcus pneu
Streptococcus pneu

Aspergillus oryzae Eucalyptus grandis Human PKDI gene. Human PKDI locus b Human adenosine Al Human secreted exp Oyster pearl prote Human cancer assoc

Aspergillus oryzae Plasmid pMT1802 en

Searched:

Database

Result Š.

Seguence:

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Trichoderma harzia

Human neurogenic d Human gene express Human adenosine Al

AgfA sequence. Sa Salmonella enterit Salmonella enterit AgfA::PT3#1 DNA se AgfA::PT3#5 DNA se AgfA::PT3#5 DNA se AgfA::PT3#7 DNA se AgfA::PT3#9 DNA se AgfA::PT3#9 DNA se

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/product - Hypersensitive_response_elicitor_protein
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AAF72217
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AAX53491
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AAX09007;
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RESULT
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DNA encoding a hyp
Bacillus sp strain
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Bacillus lichenifo
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9736.931 Million cell updates/sec
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M. tuberculosis an
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/SIDS1/gcgdata/geneseq/geneseqn/Na1981.DAT:
/SIDS1/gcgdata/geneseq/geneseqn/Na1982.DAT:
                                           Compugen Ltd.
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                    GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
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AAA14939
AAX24347
AAD00673
AAA14943
AAV59479
AAX89484
AAX89484
AAX19440
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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                                                                    The hypersensitive response eliciting protein (hrp) or polypeptide is produced as part of an active defense by plants against incompatible pathogen infections. The hypersensitive response is rapid localised necrosis. The hrp protein and gene when used in nucleotide constructs are useful for providing disease resistance to plants, insect control to plants, and enhancing plant growth (enhancing fruit size and earlier colouration and maturation), by direct application of the protein to plants, or by producing transgenic plants or seeds using the hrp gene.
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                 New Erwinia amylovora hypersensitive response eliciting gene and protein - useful for providing transgenic plants and seeds with enhanced growth, and insect and disease resistance
                                                                                                                                                                                             DB 20; Length 1344;
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/product= "Hypersensitive response elicitor"
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                                                                                                              The patent discloses a method to impart stress resistance to plants by applying a hypersensitive response elicitor in a non-infectious form to a plant or seed. The present sequence is a DNA encoding hypersensitive response elicitor protein from Erwinia amylovora. The protein is heat stable, protease sensitive and suppressed by inhibitors of plant metabolism. The present sequence is used to transform transgenic plant
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                                                                 Application of a hypersensitive response elicitor protein to
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tive 0; Mismatches
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CORP
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                                                                                                                                                                                                                                                                                                   The present sequence encodes a hypersensitive response elicitor polypeptide. The specification describes hypersensitive response elicitor polypeptide fragments, which do not elicit a hypersensitive response. Instead, the protedia impart disease resistance to plants, capaments and/or control insects. The polypeptide fragments and be used to these properties to plants. The plants which may be treated in this way include vegetables, crops and ornamental plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potents, seet potato, bean, pea, chicory, lettuce, canner, spanse, brussel sprout, beet, parsnip, turnip, cauliflower, broccoli, radish, splmach, onlon, garlic, eggplant, pepper, celry, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, carrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, cottus, strawberry, grape, raspberry, pineapple, soybean, tobacco, cottus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum or sugarcane, Arabidopsis thaliana, Saintpaulia, petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia.
                                                                                                                                                                                        Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plants, especially vegetables and ornamental flowers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1344 BP; 343 A; 372 C; 357 G; 272 T; 0 other;
                                                                                                                                                                                                                                                                   Disclosure; Page 11-12; 100pp; English.
                                                                                           H, Niggemeyer JL;
                                                       BIOSCIENCE CORP
                 98US-0103050
                                                                                                                               WPI; 2000-303745/26.
P-PSDB; AAY84855.
                                                       (EDEN-) EDEN
                 05-OCT-1998;
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ö 120 120 180 180 240 240 300 300 360 360 420 420 480 480 540 .09 9 Gaps ggggacaacgggcttggtggtcataatgcaaattctgcgttgggggcaacaacccatcgat aacgettggcggcctgaacggacgaaaaggcacagcaggaaccactccgcagtctgacagt cagggcggcgggcagatcggcgataatcctttactgaaagccatgctgaagcttattgca cgcatgatggacggccaaagcgatcagtttggccaacctggtacgggcaacaacagtgcc atgicaattettaegettaacaacaataeetegteeteggetetgiteeagteegg cggcaaaccattgagcaaatggctcaattattggcggaactgttaaagtcactgctatcg ccacaatcaggtaatgcggcaaccggagccggtggcaatgaccagactacaggagttggt ccacaatcaggtaatgcggcaaccggagccggtggcaatgaccagactacaggagttggt cagggcggcgggcagatcggcgataatcctttactgaaagccatgctgaagcttattgca cgcatgatggacgacaaagcgatcagtttggccaacctggtacgggcaacaacagtgcc Length 1344; 0; Indels 21; ; 0 В Score 1344; I Pred. No. 0; ; Mismatches ö 100.0%; 100.0%; Query Match 100. Best Local Similarity 100. Matches 1344; Conservative 121 241 61 61 121 181 241 301 181 361 301 361 421 421 481 셤 ç g ò 合 õ ద ô g õ g õ g ò g 8.

1080 1140 960 540 780 840 840 900 960 tetteceggtaettetteatetggeggtteeeettttaaegatetateaggggggaaggee aaaatagacaatctgcacgtcaccaacgtgggtgaggacgcgattaccgttaagccaaac tttggtacttttgtacgcactaacggcggtcaacagggtaactgggatctgaatctgagc ccttccggcaactccccttccggcaactactctccgtcagtaccttctcaccccatcc ggcagcacgccggtaaccgatcatcctgaccctgttggtagcgcgggcatcggggccgga ggcagcacgccggtaaccgatcatcctgaccctgttggtagcgcgggcatcggggccgga aattoggtggccttcaccagcgccggcgctaatcagacggtgctgcatgacactacc agcgcgggcaaaaaatcccacgttgaaatcactaacagttccttcgagcacgcctctgac aagatcctgcagctgaatgccgatactaacctgagcgttgacaacgtgaaggccaaagac tttggtacttttgtacgcactaacggcggtcaacagggtaactgggatctgaatctgagc cetteceggeaactececttecggeaactactetecegteagtacetteteaececeatee 83 Hypersensitive response elicitor; dspE gene; HrpW; transgenic plant; disease resistance; insect resistance; Hypersensitive response elicitor HrpW dspE gene gccaacctgaaggtggctgaatga 1344 ВР Pseudomonas syringae pv. tomato DNA; 1729 (first entry) AAX24347 standard; 07-JUN-1999 AAX24347; 1021 1021 1081 1141 1141 1201 481 601 199 841 901 1081 1261 541 661 721 721 781 781 841 961 961 1201 1261 1321 AAX24347 δy 셤 ò g á g ö g ö 셤 δ q

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pv. tomato DC3000 that codes for a 42.9 kDa hypersensitive response
elicitor (HRE) polypeptide (see AM97851), termed HrpW. To identify
any HRE-like genes in the P. syringae pv. tomato DS3000 DNA flanking
hrpR, cosmid pCPP2357, which contains this region in vector pCPP47,
the hread polypeptide (see AM97851) the ability to promote
screened for 2 potential HR phenotypes: (1) the ability to promote
tobacco HRE activity in Pseudomonas fluorescens cells carrying
to PCPP224, a delhrpz PHIT11 derivative, and (ii) interference with
the HRE activity of P. fluorescens cells carrying valid-type pHIR11.
No subclones had the first phenotype, but one, pCPP2373, had the
scoond. Transcriptional unit V of this subclone contained the
contained DNA molecule can be used to impart disease resistance to
plants, to enhance plant growth and/or to control insects on
plants. This is achieved by applying the HRE protein in a
non-infectious form to plants or plant seeds. Alternatively,
the property of plant seeds transformed with DNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1079 gecggeaagateaatgtggtgaaagacaccateaaggteggegetggegaagtetttgae 1138
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                                                                                                                                                                                                                                                             New hypersensitive response eliciting (dspE) gene and protein useful for providing transgenic plants and seeds with enhanced growth, and insect and disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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         Location/Qualifiers
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Matches 330; Conserv
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                                                             WO9907207-A1
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Pseudomonas syringae hypersensitive response elicitor encoding dspE gene.
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                                                      1093 ctgaatgccgatactaacctgagcgttgacaacgtgaaggccaaagactttggtactttt
1379 gtcactaatctgaacatcaagaacagcagtgccaaaggtgcagacgacaaggttgtccag
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Pred. No. 9.6e-37;
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57.1%;
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P-PSDB; AAY71098.
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Best Local Similarity
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plant; dspE gene;
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                  745 ggcgctaatcagacggtgctgcatgacaccattaccgtgaaagcgggtcaggtgtttgat 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "hypersensitive response elicitor protein'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypersensitive response; insect control; disease resistance; hypersensitive response elicitor; plant growth; vegetable; crop; ornamental plant; ss.
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Mismatches 233; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a hypersensitive response elicitor protein.
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Matches 330; Conservative
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The present sequence encodes a hypersensitive response elicitor polypeptide. The specification describes hypersensitive response elicitor polypeptide fragments, which do not elicit a hypersensitive elicitor polypeptide fragments impart disease resistance to plants, enhance plant growth, and/or control insects. The polypeptide fragments may be used to these properties to plants. The plants which may be treated in this way include vegetables, crops and ornamental plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower, peanut, corn, potato, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parship, turnip, cauliflower, broccoli, radish, spinach, onion, garlite, eggplant, pepper, carrot, squash, pumpkin, zucchini, cucumber, apple, pean, tobacco, citrus, strawberry, grape, raspberry, plneapile, soybean, tobacco, comato, sorghum or sugarcane, Arabidopsis thaliana, Saintpaulia,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gcagaagacggtaagttctcgttcgttaaaagcgatagcgaggggtaaacgtcaatacc 1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1079 gccggcaagatcaatgtggtgaaagacaccatcaaggtcggcgctggcgaagtctttgac 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia
                                                                                                                                                                                          Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plants, especially vegetables and ornamental flowers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctgcacgtcaccaacgtgggtgaggacgcgattaccgttaagccaaacagcgcgggcaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 233; Indels
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                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 25-26; 100pp; English.
Fan H, Niggemeyer JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.5%;
Best Local Similarity 57.1%;
Matches 330; Conservative (
                                                                            2000-303745/26.
                                                                                                                  P-PSDB; AAY84859
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The present sequence encodes a pectic acid lyase isolated from microorganism Bacillus sp. KSM-P15. The pectic acid lyase has high pectic acid lyase activity which degrades pectin in plant cell walls and fibre in vegetables, and so is useful as a component of detergents a food-processing agent, or a fibre-processing agent. The pectic acid
                                                                                                                                                    1051 actaacagttccttcgagcacgcctctgacaagatcctgcagctgaatgccgatactaac 1110
                                                                                                                                                                                                                                                                                      1171 caacagggtaactgggatctgaatctgagccatatcagcgcagaagacggtaagttctcg 1230
                                        409 accacctacaaagtggtgatgaacgtggaaaactgcaacatttccagagtgaaggatgcg 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus sp. KSM-P15; pectic acid lyase; pectinic acid lyase; pectin; detergent; food-processing; fibre-processing agent; cell wall; ds.
                                                                                                                                                                                                                  New Bacillus pectic acid lyase – useful as a detergent component, food-processing agent and a fibre-processing agent
                                                                                       ggtgaggacgcgattaccgttaagccaaacagcgcgggcaaaaaatcccacgttgaaatc
                                                                                                                                                                                     289 tcgggcgggggagcctacaaggcgtatgacaaggtgttccaaatcaatgcagcgggacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..591
/*tag= a
/note= "no stop codon given"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KAOS ) KAO CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yoshimatsu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caaaccttcaccgccggttcaga---attaggcgatggcggccagtctgaaaaccagaaa 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 cagacctatgtggctaatccgaatacattgggggacggatcgcaggcggagaatcagaag 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detergent composition containing protopectinase active at alkaline PH - on protopectin and polygalacturonic acid, provides better removal of muddy soil
                                                                                                                                                                                                               Bacillus sp. strain KSM-P15; pectic acid lyase; protopectinase; protopectin; polygalacturonic acid; detergent; cotton; surfactant; cellulase; protease; bleaching agent; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 591;
                                                                                                                                                                                 Bacillus strain KSM-P15 pectic acid lyase encoding DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koike K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%; Score 94.8; DB 19;
1larity 52.8%; Pred. No. 1.1e-18;
Conservative 0; Mismatches 217;
1619 ggcaacatcgccatgaccgacgtcaaacacgcctacga 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kasai M, Kobayashi T, Koike
tsu A, Tsumadori M, Wada Y;
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..591
/*tag= a
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                                                                                   ВР
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                                                                                 AAV69879 standard; DNA; 591
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                                                                                                                                                  (first entry)
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Suzumatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-568339/48.
P-PSDB; AAW83014.
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Best Local Similarity
Matches 263; Conserv
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                                                                                                                                                                                                                                                                                 Bacillus sp
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Shikata S,
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lyase has a higher optimum reaction pH (10.3-10.7) than known Bacillus pectic acid lyases (PH 8-9.5) and so has wider industrial applications. Unlike present pectic acid lyases, the new enzyme has a high enzyme activity, and can be produced on a mass scale.
                                                                                                                                                                                                                                                                                                                                                                                                                                             ctgagcgttgacaacgtgaaggccaaagactttggtacttttgtacgcactaacggcggt 1170
                                                                                                                                                                                                                                                                                                                                                ggtgaggacgcgattaccgttaagccaaacagcggggggaaaaatcccacgttgaaatc 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caacagggtaactgggatctgaatctgagccatatcagcgcagaagacggtaagttctcg 1230
                                                                                                                                                                                                                                                                                                                                                                                                           289 tcgggcgggcagcctacaaggcgtatgacaaggtgttccaaatcaatgcagcggggacg 348
                                                                                                                                                 cagacggtgctgcatgacaccattaccgtgaaagogggtcaggtgttgatggcaaagga 813
                                                                                                                                                                                                 caaaccttcaccgccggttcaga---attaggcgatggcggccagtctgaaaaccagaaa 870
                                                                                                                                                                                                                                                  ccgctgtttatactggaagacggtgccagcctgaaaaacgtcaccatgggcgacgaggg 930
                                                                                                                                                                                                                                                             goggatggtattcatctttacggtgatgccaaatagacaatctgcacgtcaccaacgtg 990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 atcaacattcgtaacttcagggccgatgacatcgggaagctggttcggcagaacggaggc 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accacctacaaagtggtgatgaacgtggaaaactgcaacatttccagagtgaaggatgcg 468
                                                                                                                                                                                                                        cagacctatgtggctaatccgaatacattgggggacggatcgcaggcggagaatcagaag 123
                                                                                                                          Gaps
                                                                                                                                                                         4 ccgacggtcgttcatgaaacgattcgtgtgcctgccggtcagacgtttgacggaaaaggg 63
                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                Length 591;
                                                                                               Similarity 52.8%; Pred. No. 1.1e-18; Conservative 0; Mismatches 217; Indels
                                                           Sequence 591 BP; 160 A; 137 C; 176 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus licheniformis DNA encoding pectate lyase I.
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/*tag= a
/product= "Pectate lyase I"
/FC_number= "4.2.2.2"
82..663
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                                                                                               Query Match 7.1
Best Local Similarity 52.8
Matches 263; Conservative
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AAX89484
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The present sequence is a DNA encoding pectate lyase I. It is a pectin degrading enzyme derived from Bacillus licheniformis, ATCC 14580. The enzyme comprises a catalytic active domain and a cellulose binding domain (CBD) that are operably linked to each other. It shows optimum activity at pH greater than 9 and temperature 55 degree centigrade. It can be used in detergent compositions, for improving the properties of callulosic fibres, yarn, woven or non-woven fabric, for the degradation of plant material e.g. recycled waste paper, mechanical paper-making pulps or fibres subjected to rettling process, for preparing animal feed and for processing wine or juice. DNA encoding the enzyme can also be used for the production of transgenic plants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 gotgattgcaggtccggagctcggggacggcagccaacgcgaggatcaaaaaccgatttt 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 666 BP; 205 A; 136 C; 178 G; 147 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Schnorr K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.5%; Score 74.2; DB 20;
llarity 55.7%; Pred. No. 2e-12;
Conservative 0; Mismatches 113;
/*tag= b
/function= "Pectin degradation"
                                                                                                                                                                                                                                                                                                                                                                                                                      Lange NEK,
                                                                    /*tag= c
/label= Pro-sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated pectate lyase enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Page 79; 93pp; English.
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                                                                                                                                                                                                                                                                                           97DK-0001344
98US-0073684
                                                                                                                                                                                                                                             98WO-DK00514
                                                                                                                                                                                                                                                                                                                                                                                                                      Bjornvad ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgcgattaccgttaa 1013
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P-PSDB; AAY28446.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Andersen LN,
                                                                                                                                                                                                                                                                                           24-NOV-1997;
06-MAY-1998;
                                                                                                                                                                                                                                             24-NOV-1998;
                                                                                                                                            WO9927083-A1
                                                                                                                                                                                             03-JUN-1999
                                             sig_peptide
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Matches 142;
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                                                364 ggtgctgaccagattgagggtgtgcactgcgagggttcttgcaccattgagaacgtctgg 423
                                                                                                                                                                                                                                                                                                                                                 ggcgacgacggggcggatggtattcatctttacggtgatgccaaaatagacaatctgcac 978
                                                                                                                                                                                                            1039 cacgitigaaatcactaacagiticciticgagcacgccitigacaagatccigcagcigaat
                                                                                                                                                                                                                                         482 -----aggtcattggcggtggtgcccagggcgccgatgacaaggtcatccagcacaac
                                                                                                          424 tggcaagaggtctgcgaagacgccctcaacttcaagggtaccggcaccggcgtccaca--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis; M. tuberculosis; antigen; immuno
immunotherapy; diagnosis; immunisation; vaccine; infection;
immune response; skin test; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. tuberculosis antigen 3' Erdsn-7 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ19440 standard; cDNA; 1166 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-527409/44
                                                                                                                                                                                                                                                                                                                                                                                                                        1159 actaacggc 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595 teetgegge 603
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Lodes MJ, Reed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ19440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
                                                                                                       979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for monitoring differential cexpression of genes in a first filamentous fungal (FF) cell relative to expression of genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS care used in the methods for monitoring differential expression of genes (in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring che global expression of genes from FF cells allows the production potential of the microcyganisms to be improved. New genes may be consible functions of unknown open reading frames can be discovered, possible functions of unknown open reading frames can be considered. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore control of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore confined in the stress one spot on an example of the results. Astilated several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an erray equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate canalysis of the results. Astilates to AAF11487 represents ESTS from Aspergillus oryzae; and AAF14879 to AAF14879 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                                                                                                                          expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Olsen PB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clausen IG,
                                                                                                       Multiple gene expression; filamentous fungal cell; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 732 BP; 151 A; 240 C; 193 G; 147 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kauppinen S,
                                                   Aspergillus oryzae EST SEQ ID NO:4856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 2050; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shuster JR,
                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAR-2000; 2000WO-US07781.
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(first entry)
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) NOVO NORDISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rey MW,
                                                                                                                                                                                                                                                             Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                             WO200056762-A2.
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13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                 28-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 88;
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(NOVO
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(first entry)

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The present invention describes polypeptides comprising an immunogenic part of a Mycobacterium tuberculosis antigen (Ag). Also described are vaccines and fusion protein containing M. tuberculosis Ag's.

M. tuberculosis Ag's, DNAs encoding them, derived fusion proteins and other polypeptides fragments, can be used in pharmaceutical compositions or vaccines to generate a protective or therapeutic immune response to M. tuberculosis and as reagents in skin tests for diagnosis of tuberculosis. Ag can induce proliferation of, or cytokine secretion by, T. B or natural killer cells and/or macrophages in tuberculosis-immune subjects. AAZ19249 to AAZ19460 and AAX39083 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY39225 are used in the exemplification of the present invention.
New antigens from Mycobacterium tuberculosis useful in diagnostic skin tests and protective or therapeutic vaccines or compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1166 BP; 117 A; 371 C; 121 G; 207 T; 350 other;
                                                                                                                                                                                       Claim 4; Page 259; 299pp; English.
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Indels

Score 46.6; DB 21; Pred. No. 0.00047; 0; Mismatches 184;

Ouery Match 3.5%; Best Local Similarity 47.7%; Matches 176; Conservative

Length 732;

tttgatggcaaaggacaaaccttcaccgccggttcagaattaggcgatggcggccagtct 858

tatgatggtggcatgaagaccttcggccgtggtgtcaagtgtaccggtcagaaggagggt

244 199

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859 304

Houghton R;

Dillon DC, Hendrickson RC, House, SG, Skeiky YAW, Twardzik DR,

99WO-US03268 98US-0072967 98US-0025197 tytnnccamcmcsctctmtcmaactckccggyckcncmyctctckccaynmaacckkty 622

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                                                                                                                              : | :: :: |: :| :: |: cywcnwycymyckckcagwyknmctccwactctmyntttctctcnkcccmkaccknttct 682
                                                                        508 teceettttaaegatetateaggggggaaggeeeetteeggeaaeteeetteeggeaae 567
                                                                                                                                                                                     448 tttggccaacctggtacgggcaacaacagtgcctcttccggtacttcttcatctggcggt 507
                                                                                                                                                                     568 tactctcccgtcagtaccttctcacccccatccacgccaacgtcccctacctcaccgctt 627
                              Gaps
                                                                                                                                                                                                                          628 gatttcccttcttctcccaccaaagcagccggggggcagcaccggtaaccgatcatc 685
                                                                                                                                                                                                                                        Antigen; diagnosis; detection; infection; antibody; immunisation;
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Length 1166;
                                                                                                                                                                                                                                                                                                                                                                                                            . M. tuberculosis recombinant antigen cDNA encoding 3' Erdsn-8.
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                             Indels
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 DB 20;
                          55; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on DC, Hendrickson RC, Ho
Skeiky YAW, Twardzik DR,
             0.0086;
3.2%; Score 42.8;
28.6%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                          AAZ19228 standard; cDNA; 1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0072596
98US-0024753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis:
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                             68; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immunity; ss.
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Lodes MJ, Reed SG,
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              Similarity
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 Query Match
              Best Local
Matches 6
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Epstein Barr Virus Nuclear Antigen 1 DNA; plasmid pCMVEBNA; EBNA 1; episome; transfection; origin of replication; EBV oriP; receptor; eucaryotic host cell; recombinant cell line; ion channel; gene therapy; multiple gene expression; transporter protein; transcription factor; adheaion molecule; antisense therapy; gene amplification; cell immortalisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a DNA encoding Epstein Barr Virus Nuclear Antigen 1 (EBNA 1), which is obtained from commercially available plasmid pcwNeshN. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (oriP) and a gene encoding protein or RNA of interest. Eucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant protein are pressing multiple genes of interest. This provides a rapid and reliable method of stably expressing multiple genes in transfected cells. The episomes are useful in the transfection of genes
                                   cywcnwycymyckckcagwyknmctccwactctmyntttctctctcnkcccmkaccknttct 682
                                                                                                      683 cwcscccccacakaymcyawcmtmtccmctckacscccyycnnyccmnmcwcmtcwctw 742
 508 tocoottttaacgatotatcaggggggaaggcooottooggcaactoooottooggcaac 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a 5
                                                                                                                                        gatttcccttcttctcccaccaaagcagccggggggggagcaccggtaaccgatcatc 685
                                                                                                                                                                      743 nakcancuttcttctctcmmymtmackcwcnntcnccksgaccytctcactkmkcckm 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_except= (pos:799..800, aa:Gly)
//tote= "The sequence is described throughout the
specification as being 1926 uncleotides long, but sequence of only 1925 bp has been given in figure
                                                                    tactetecegteagtacetteteacececatecaegecaaegteecetaceteaegett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New method for expressing genes from recombinant eukaryotic cells, useful for gene therapy {	extstyle -}
                                                                                                                                                                                                                                                                                                                                                               Epstein Barr Virus Nuclear Antigen 1 (EBNA 1) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robbins AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "EBNA 1"
                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                             17-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB, Horlick RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-610610/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Epstein-barr virus.
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3.2%; Score 42.8; DB 20; Length 1166; 28.6%; Pred. No. 0.0086; iive 55; Mismatches 115; Indels 0;

Query Match 3.29 Best Local Similarity 28.6 Matches 68; Conservative

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P-PSDB; AAW72063, AAW72064, AAW72065, AAW72066
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Plougastel B, Thomas G,
                                                                                                                                                                                                  Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyA_signal
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                                                                                                                                                                                                                                                                                                                                                 AAQ50643;
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                  Herpes
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       molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, for gene amplification, cell immortalisation, etc.
                                                                                                                                          600 cacgccaacgtcccctacctcaccgcttgatttcccttctccccaccaagcagccgg 659
                                                                                                         ccettccggcaactccccttccggcaactactctcccgtcagtaccttctcacccccatc 599
                                                                                                                     encoding receptors, transporter proteins, ion channels, adhesion
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                                                                       Length 1925;
                                                                                                                                                                                                                                                                                                                    HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                         /product="ORF#1 protein"
/hote="encoded protein shown in AAW72063"
1282..2442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW72065"
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                                          Sequence 1925 BP; 486 A; 352 C; 872 G; 215 T; 0 other;
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/product= "ORF#2 protein"
/note= "encoded protein shown
complement (2699.3625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "encoded protein shown complement (3564..4280)
                                                                     Score 38.2; DB
Pred. No. 0.28;
0; Mismatches
                                                                                                                                                                                         753 TCCTGCCCTCCTGCTCCTGCCCTCCTGCTG 719
                                                                                                                                                                                                                                                                                                  HSV-2 strain SB5 Contig ID 93 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product- "ORF#3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "ORF#4 protein"
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527..1627
/*tag= a
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                                                                                                                                                                                                                                            AAV62147 standard; DNA; 4289
                                                                     2.8%;
ilarity 52.9%;
Conservative
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96US-0030279.
                                                                                                                                                                                                                                                                                                                                               simplex virus type 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leary JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-286847/25
                                                                     Query Match
Best Local Similarity
Matches 82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-OCT-1997;
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04-NOV-1996;
               can also be
for gene amp
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Esser KM,
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This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain SB5 (deposited as ATCC VR-2546), is designated Contig ID 93, and encodes 4 HSV-2 proteins. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 CCTCCCCTCTCCACCTCCTAATCTTACTTTTCTCCCTCTCCCCTATTTCTCCCCTCCCTTCC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 cettecggcaacteceettecggcaactactetecegteagtacetteteaceeeeee 600
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bes simplex virus type-2 sequences - useful in, e.g. prevention treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ews gene; malignant melanoma; hum-fil.1;
primitive peripheral neuroectodermal tumour; human chromosome 11;
human chromosome 22; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Ews gene clone BF1AC5 from foetal brain cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4289 BP; 710 A; 1360 C; 1568 G; 643 T; 8 other;
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2143..2148
/*tag= b
2331.2336
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601 acgccaacgtcccctacctcaccgcttgatttcccttcttctcccacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.8%; Score 37.6; DB 19;
59.3%; Pred. No. 0.64;
tive 0; Mismatches 44;
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/product= EWS_protein
                                                                                                                          Claim 1; Page 288-289; 748pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
25..1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ50643 standard; cDNA; 2371 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CNRS ) CNRS CENT NAT RECH SCI.
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The probes 22RR3 and 22RR12 were used to screen a human foetal brain cDNA library (Stratagene cat.# 936206). The clone BFIAC5 was identified and sequenced. It represents the entire coding region and 3'-UTR of the Ews gene.
                                                            New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence involved in chromosomal trans-location, also derived mRNA, probes, fusion proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma
                                                                                                                                                         Disclosure; Fig 6; 123pp; French.
            WPI; 1993-386580/48.
P-PSDB; AAR44555.
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Sequence 2371 BP; 639 A; 587 C; 659 G; 486 T; 0 other;

ö 1969 GACGGIGCTCGCCTTTATCCATTTTTCCAGGTCCTCCACGTCCTCCTCTTCTTCCAG 1910 . 1909 TCTGTTCCATCAAAGGTCCAGGGGCCCCCCAGGGCCACCTCGTCTTCCTCCACAAAGC 1850 1849 CACCTCGGTCCATGCCCCGGCCACCACGGAAGCCACCTCTGTCTCCACCACCACCACCTC 1790 1789 TGAACATTCCACGGGACCACCACGATCCATGAGGCCACCTCTTCCTCCCCGCATGCAC 1730 654 agccgggggcagcacgccggtaaccgatcatctgaccctgttggtagcgcggggcatcgg 713 534 gaaggecetteeggeaacteeetteeggeaactacteteegteactteteace 593 594 cccatccacgccaacgtccctacctcaccgcttgatttcccttctccccaccaaagc 653 714 ggccggaaattcggtggccttcaccagcgccggcgctaatcagacggtgctgcatgacac 773 0; Gaps Query Match

2.8%; Score 37.4; DB 14; Length 2371;
Best Local Similarity 47.0%; Pred. No. 0.54;
Matches 116; Conservative 0; Mismatches 131; Indels 0; Dp g g g ò ò ò

774 cattacc 780

1729 CAGGGCC 1723

Search completed: October 21, 2001, 11:33:28 Job time: 2576 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

, Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. The Washington Univ. Nematode EST project, 1999	AL Unpublished (19 Contact: McCart The Washington Washington 444 Forest Par Tel: 314 286 18 Fax: 314 286 18	Email: est@watson.wustl.edu The library was constructed by Brandi Chiapelli and Dr. James The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. Seq primer: custom 5' primer (pAMP1_5'_47) High quality sequence stop: 455. Location/Qualifiers Source 1. 469 Annahism="Herberodera glycines"	/db_xref="taxon:51029" - 7	Charlie Opperman of North Carolina State University (see Genetics, 146:1311-8, 1997). Frozen J2 nematodes were provided by Dr. Rick Davis also of NCSU. Special thanks to Dr. Yulia Korshunova from the Lovett Lab at Washington University in St. Louis for helping with methods." BASE COUNT 144 a 96 c 124 g 104 t lothers	Query Match 4.7%; Score 63.8; DB 152; Length 469; Best Local Similarity 53.5%; Pred. No. 2.6e-07; Matches 154; Conservative 0; Mismatches 133; Indels 1; Ga	 Qy 815 aaaccttcaccgccggttcagaattaggcgatggcggccagtctgaaaaccagaaaccgc 874 	242 IGATCCGTGCCGAAAAGAATGCAGTGATCAAAAATTTGATCATTGGCCAAAACGGGGCGG	Oy 935 atggtattcatctttacggtgatgccaaaatagacaatctg-cacgtcaccaacgtgggt 993	aacagttccttcgagcacgcctctgacaagatcctgcagctgaatgcc 1101 	RESULT 2 CNSO06ON/C LOCUS CNSO06ON 910 bp DNA GSS 03-JUN-1999 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
SUMMARIES Result Query No. Score Match Length DB ID Description	1 63.8 4.7 469 152 BG310823 BG310823 47 3.5 910 219 CNGO0GON AL055629 43.4 3.2 844 219 CNSO08MZ AL052079 4 43.4 3.2 844 219 CNSO052P AL052079 4 42.8 3.2 782 80 BF280877 Bf280877 6 42.8 3.2 782 153 BG447322 BG447322	7 41.8 3.1 1260 170 BF866129 8 41.6 3.1 538 105 AL514267 9 41.6 3.1 870 165 BE258873 11 41.2 3.1 975 220 CNSOXRBD 12 41.2 3.1 391 152 BG310856 13 41.2 3.1 534 112 AW173078 14 41.2 3.1 563 19 AI356664 15 41 3.1 667 106 AL565523 16 40.8 3.0 669 228 AO447577	17 40.8 3.0 977 219 CNSOOJX7 ALD76850 18 40.4 3.0 812 220 CNSOAJGO AL200193 20 40.2 3.0 551 11 AA771081 AA701081 21 40.2 3.0 552 11 AA771081 AL238257 22 40.2 3.0 101 219 CNSOBEDF AL238257 23 40 3.0 101 219 CNSOBEDF AL068951 24 39.8 3.0 14 AA966471 AA966471 AA966471 25 39.8 3.0 667 168 BF700488 BF700488 BF700488 26 39.8 3.0 667 168 B7331220 AQ331220 27 39.6 2.9 539 251 AZ999203 AZ9994463 28 39.6 2.9 793 256 B18549 B18549 T18	-29 39.6 2.9 995 219 CNSO1BMR AL109533 31 39.4 2.9 1072 221 CNSO1BMS AL20602 31 39.4 2.9 1072 221 CNSO1BMS BE572645 BE572645 32 39.2 2.9 968 147 BF341280 BF341280 BF341280 33 39.2 2.9 1095 220 CNS02762 AL184292 35 39 2.9 619 222 FR0007731 AW732191 291541 £ 291541	39 2.9 1101 219 CNSOZABE BF68247 39 2.9 1101 219 CNSOZBI ACROSPA 77 86.9347 38.8 2.9 398 152 BG356477 BG356477 BE601363 BE601363	42 38.8 2.9 568 154 BG463697 43 38.8 2.9 573 119 AW679673 44 38.8 2.9 597 152 BG323139 45 38.8 2.9 626 152 BG355747	ALIGNMENTS	RESULT 1 BG310823 LOCUS BG310823 469 bp mRNA EST 05-APR-2001 DEFINITION ro43410, yl Heterodera glycines J2 pAMPl v2.1 Chiapell1 McCarter Heterodera glycines cDNA 5' similar to TR:Q9x622 Q9x622 PECTATE LYASE PRECURSOR; mRNA sequence.	ACCESSION BG310823 VERSION BG310823.1 G1:13112624 KEYWORDS EST. SOURCE Actorders glycines.	

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DAMP1: The library was constructed by and Dr. James McCarter at Washington
L. Louis. The cDNA was made by using Dynabead
and (Dynal). PCR based library using a
col, from the SWART PCR cDNA Synthesis Kit
Directionally cloned into the UDG sites of
as are the OPG strain developed by Dr.
and North Carolina State University (see
:1311-8, 1997). Frozen J2 nematodes were
Rick Davis also of NCSU. Special thanks
orshunova from the Lovett Lab at Washington
St. Louis for helping with methods."
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Similarity
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Web: www.genoscope.cns.fr.

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/db_xref="taxon:7227"
/clone_lib="RPCI-98" ·
/clone="BACR14J21"
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Conservative 148; Mismatches 179;
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19.3%; Pred. No.
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- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
                             Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR17K04 of RPCI-98 library from Drosophila melanogaster (fruit
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BACR11P16 of RPCI-98 library from Drosophila melanogaster (fruit
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                                                                        - Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

- Web: www.genoscope.cns.fr.

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Pl and EST libraries. A more detailed description of the library
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found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                 Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR11P16"
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Best Local Similarity 19.3%; Pred. No. 0.21;
Matches 57; Conservative 117; Mismatches 122;
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20-NOV-2000 (Rel. 65, Last updated, Version 1)
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Wing R.A., Frisch D., Yu Y., Main D., Rambo T., Simmons J., Henry D.,
Wood T.C., Leslie A., Wilkins T.A.;
"An integrated analysis of the genetics, development, and evolution of the
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvacea; Gossyptum.
1 (bases 1 to 782)
Wing, R.A., Frisch, D., Yu, Y., Maln, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
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/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
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/db_xref="ESTLIB:2480"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
/organism="Gossypium arboreum"
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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61.8%; Pred. No. 0.31;
ilve 0; Mismatches
                                                                                                                                                                                                                                                                                                                            Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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High quality sequence start: 3
High quality sequence stop: 742.
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BG447322.1 GI:13356974
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Homo sapiens
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Chlamydomonas reinhardtil.

Chlamydomonas reinhardtil

Eukaryota: Viridiplantae: Chlorophyta; Chlorophyceae; Volvocales;

Chlamydomonadacee; Chlamydomonas.

I (bases 1 to 1260)

S Grossman,A., Davies,J., Federsplel,N., Harris,E., Hauser,C.,

Lefebvre,P., McDermott,J.P., Shrager,J., Sliflow,C. and Stern,D.,

Analyses of the Chlamydomonas reinhardtil Genome: A Model,

Unicellular System for Analyzing Gene Function and Regulation in

Vascular Plants; project phase 3

Unpublished (2000)

L. Contact: Charles Hauser

Contact: Charles Hauser

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963066G03.x1 C. reinhardtii CC-1690, Stress condition I, normalized
, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
BF866129
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/organism="Chlamydomonas reinhardtii"
/organism="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
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/tlone_ltpe="Fibers isolated from bolls harvested 7-10
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Pred. No. 0.31;
0; Mismatches 42; Indels 0;
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Fax: 8
                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Gossypium arboreum"
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99 c 361 g 13
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Best Local Similarity 61.8'
Matches 68; Conservative
Unpublished (2000)
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XhoI; This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP-N (30 min, lhr, 4hr), TAP-S (30 min, lhr, 4hr), TAP-S (30 min, lhr, 4hr), TAP-S (30 min, lhr, 4hr) and NH4 to (ND3 (30min, lhr, 4hr). PolyA mRNA was purified from each sample, pooled and CDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoRI (3') sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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/clone_lib="LTI_NEUOG_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/clone_lib="LTI_NEUOG_PL2"
/fissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_l: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com"

3 a 299 c 103 g 85 t 48 others
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqreféquenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   599 ccacgccaacgtcccctacctcaccgcttgatttcccttctcccc 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41.8; DB
Pred. No. 0.69;
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/organism="Homo sapiens"
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/clone="CLOBB0072D09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%;
illarity 45.5%;
Conservative
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         CNSO2KBD 975 bp DNA GSS 14-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
145K19 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Actinopterygii; Neopterygii; Teleostel; Euteleostel; Neoteleostel; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

[ (bases l to 975)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                 539 ccccttccggcaactccccttccggcaactactctcccgtcagtaccttctcaccccat 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="G"
/note="Genoscope sequence ID : COAG145AF10SP1-end
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//Organism="Tetraodon nigroviridis"
//db.ref="taxon:99883"
/clone="145K19"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 870)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE258873 870 bp mRNA EST 13-JUL-2000 601116824F1 NIH_MGC_16 Homo sapiens CDNA clone IMAGE:3357533 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ArCc
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM164 row: o column: 06.
Location/Qualifiers
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                                                                                              cccttccggcaactccccttccggcaactactctcccgtcagtaccttctcacccccat 598
                                                                                                                                  449 ttggccaacctggtacgggcaacaacagtgcctcttccggtacttcttcatctggcggtt 508
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Pred. No. 0.7;
0; Mismatches 99; Indels 0;
                  Length 538;
                  DB 105;
                3.1%; Score 41.6; DB
llarity 43.1%; Pred. No. 0.61;
Conservative 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                             gaaattcggtggccttcaccagcgccggcgc
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Matches 91; Conserv
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KEYWORDS SOURCE ORGANISM

ACCESSION VERSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Seq primer: custom 5' primer (pAMPI_5'_#7)
High quality sequence stop: 353.
Location/Qualifiers
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MCGATEL, Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T.
MCGATEL, M., Marra, M., Hiller, L., Kucabo, T., Theising, B., Bowers, Y.,
Glbbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvill, R.,
Ronko, I., Kennedy, S., Magulre, L., Beck, C., Underwood, K., Stepbee
, Nonko, I., Person, B., Swallre, L., Harvey, N., Schurk, R., Schn, S.,
M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S.,
M., Allen, M., Person, P., Swaller, T., McCann, R., Waterston, R., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heterodera glycines
Eukaryota: Metazoa; Nematoda; Chromadorea: Tylenchida; Tylenchina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Heterodera glycines J2 pAMP1 v2.1 Chiapelli
                                                                                                                                                                                                                                                                                                                                                                      BG310856 391 bp mRNA EST 05-APR-2001 ro44803.y1 Heterodera glycines J2 pAMPl V2.1 Chiapelli McCarter Heterodera glycines CDNA 5' similar to TR:Q9X622 Q9X622 PECTATE LYASE PRECURSOR ;, mRNA sequence.
474 CCCCCCCSSSMCCCTTCCCCCCMCYCCCSCGCCCMTTCTSASTCSSMSCCCCSCYTCCC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fax: 314 286 1810
                                                                            659 ggggcagcacgctaaccgatcatcctgaccctgttggtagcgcgggcatcgggggccg
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
                                                                                                                                                                                 719 gaaattcggtggccttcaccagcgccggcgctaatcag 756
                                                                                                                                                                                                                  /organism-"Heterodera glycines"
/db_xref-"taxon:51029"
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BG310856.1 GI:13112657
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Length 391;

DB 152;

Score 41.2;

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Query Match

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/note="Vector: pT713D-pac (Pharmacia) with a modified
polylinker; Site_1: NO I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT773 vector. Library and Eco RI sites of the modified pT773 vector. Library constructed by Bento Soares and M. Fatima Bonaldo. " 158 c 61 g 181 t
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information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI201143 495 bp mRNA EST 27-JAN-1999 qf64g10.xl Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754850 3' similar to contains element MSR1 repetitive element ;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                               Gaps
                                                                                  852 ccagtctgaaaaccagaaaccgctgtttatactggaagacggtgccagcctgaaaaacgt 911
                                                                                                                                  223 CNAGTCGGAGGGCCAAAAAGCACTGATCCGTGCCGAAAAGGGCGGCAGTGATCAAAATTT 282
                                                                                                                                                                                           912 caccatgggcgacgacgggggggggtgtattcatctttacggtgatgccaaaatagacaa 971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D.,
, Ph.D.
                            74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.Llnl.gov/bbrp/mage/lmage.html
Insart Length: 1829 Std Error: 0.00
Seq primer: -400P from Glbco
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Pred. No. 0.77;
); Mismatches 43;
                                                                                                                                                                                                                                                                                                    972 tctgcacgtcaccaacgtgggtgaggacgcgattac 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:1754850"
/clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                                                                                                                         343 TGTGTGGTGGGAGAAGGTTGGCNAANACNCNCCAC 378
                               Mismatches
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .495
/organ1sm="Homo saplens"
/db_xref="taxon:9606"
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Location/Qualiflers
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Similarity 52.6%;
82; Conservative (
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DEFINITION

AW173078

RESULT

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ð 8 ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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CONA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. Cona Library Preparation: M. Bento Soares, Ph.D., Cona Library Arrayed by: Greg Lennon, Ph.D. Cona Library Arrayed by: Washington University Genome Sequencing Center Clone distribution: NCI-GCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: wown-bio.llnl.gov/bbrp/limage/limage.html
Insert Length: 1179 Std Error: 0.00
Seq primer: 40UP from Gibco
High quality sequence stop: 448.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pr773D-Pac (Pharmacia) with a modified Doylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as vitracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-14770983, and 1475592-1476743), Subtraction by Bento Soares and M. Fetima Bonaldo. "

176 c 67 g 207 t
                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:2009439"
/clone_lib="NCI_CGAP_GC6"
/tissue_type="pooled germ cell tumors"
/lab_host="DH108"
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Pred. No. 0.8;
0; Mismatches
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/db_xref="taxon:9606"
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AL566523
AL566523.1 GI:12918965
                                                 AI336864.1 GI:4073791
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AUTHORS
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                           ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_CGB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatina Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 534)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Glbco
High quality sequence stop: 466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           539 cccttccggcaactccccttccggcaactactctcccgtcagtaccttctcaccccat 598
312 CCTCTTCCAGCTCCTCTTCCAGCTCCTCCTCCTCCTCCTCCTCACATATTCAGCCTCTT 371
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IMAGE:2663777 3' similar to contains element MSR1 repetitive
element ;, mRNA sequence.
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Pred. No. 0.79;
0; Mismatches 43; Indels 0;
                                                                599 ccacgccaacgtcccctacctcaccgcttgatttcccttcttctcccacc 648
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/db_xref="taxon:9606"
/db_xref="Taxon:9606"
/clone=lib="Soares_NFL_T_GBC_S1"
/lab_host="DH108"
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174 c 68 q 190 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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AW173078.1 GI:6439026
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Matches 67; Conservative
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AF083620
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      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Database

U94513 Erwinia amy Y13831 Erwinia amy AF08350 Erwinia a U97504 Erwinia amy AF037983 Pseudomon AF032006 Pseudomon AF232006 Pseudomon AF233004 Pseudomon

Description

/organism="Erwinia amylovora" /strain="Ba321; ATCC 49947" /db_xref="taxon:552" /db_xref="Atxon:552" /db_xref="Atxon:552" /db_xref="astrain that infects apples, pears, and other pomaceous plants" complement(<1784) /gene="dispE" complement(<1749) /gene="dispE" complement(<1714) /gene="dispE" complement(<1714) /gene="dispE" complement(<1714) /gene="dispE" complement(<1714) /gene="dispE" /note="HTP-secreted pathogenicity/avirulence protein similar to pseudomonas syringae AvrE" /codon_start=1 /transl_table=11 /product="bsepE" /prod	/gene="dape" complement(755. 784) complement(755. 784) /gene="disease-specific operon" /note="HrpL-dependent promoter consensus sequence; hrp box" 825854 /gene="hrpW operon" /note="HrpW operon" 9252692 /gene="hrpW operon" 900905 /gene="hrpW" /note="hrpW"	·	GWWDLMISHISAEDGRFSFVKSDSEGLNVNTSDISLGDVENHYKVPMSANLKVAE" 2242247 22522547 22522547 22522547 22522547 22522547 22522547 22522547 22522547 22522547 22522547 22522540 2252255225692 26552692 /gene="http://opercol."
gene gene CDS	promoter . promoter gene RBS	CDS	RBS CDS CDS terminator
7.1 1245 1 AB011839 AF01713 Bacillus 6.8 47739 1 AF01713 Bacillus 6.8 299210 2 BSUB018 299212 Bacillus 8.4.7 1214 2 BSP237980 AJ237980 Bacillus 8.4.5 884 14 FSOPELAB AJ237980 Bacillus 8.4.5 884 14 FSOPELAB AJ237980 Bacillus 8.4.5 884 14 FSOPELAB AJ237980 Bacillus 8.4.5 884 14 FSU3305 CHUBATIUM SO 10.0049 10.00494 10.	3.0 169434 90 AL359205 3.0 17188 67 AC021198 3.0 135039 86 AC006060 3.0 135039 86 AC006060 3.0 156975 81 AL442123 3.0 192730 97 HU45743 2.9 162342 80 AL35246 2.9 166735 79 AL35861 2.9 166735 79 AL35861 2.9 90832 85 AC003065		Purpoparionogy 87, 522 (1997) 2 (bases 1 to 2708) Kim,J.F. and Beer,S.V. HrpW of Erwinia amylovora, a new harpin that contains a domain Homologous to pectate lyases of a distinct class J. Bacteriol. 180 (19), 5203-5210 (1998) 9422475 3 (bases 1 to 2708) Kim,J.F. and Beer,S.V. Direct Submission Submitted (18-MAR-1997) Plant Pathology, Cornell University, 334 Plant Science Bldg., Ithaca, NY 14853, USA 12708
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(bases 1 to 9985)
Gaudriault, S., Malandrin,L., Paulin,J.P. and Barny,M.A.
Gaudriault,S., Malandrin,L., Paulin,J.P. and Barny,M.A.
DspA, an essential pathogenicity factor of Erwinia amylovora showing homology with AvrE of Pseudomonas syringae, is secreted via the Hrp secretion pathway in a DspB-dependent way
MMOI. Microbiol. 26 (5), 1057-1069 (1997)
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1932 AGCGCGGCCAAAAATCCCACGTTGAAATCACTAACAGTTCCTTCGAGCACGCCTCTGAC
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Location/Qualifiers
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Submitted (18-MAY-1998) S. Gaudriault, INRA, 1
75231, Paris, FRANCE
Gaudriault, S., Brisset, M.N. and Barny, M.A.
HrpW of Erwinia amylovora, a new Hrp-secreted
FESS Lett. 428 (3), 224-228 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hrpW gene; promoter.
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/clone="pSG10"
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Erwinia amylovora hrpW,
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Submitted (13-JUN-1997)
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Erwinia amylovora.
Erwinia amylovora
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Gaudriault, S.
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3 (bases 1 to 9985)
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SGTGSSGGSPFNDLSGGKAPSGNSPSPSTSFPSPTSPTSPLPSPSTSTANA
AGGSTPVTDHPDPVGSAGIGAGNSVAFTSAGANQTVLHDTITVKAGQVFDGKQOFFTA
GSELGDGGGSENQKPLFILEDGASLKNVTMGDDGADGIHLYGDAKIDNLHVTNVGEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOOKRHOLNNEGOMROTMLSKWAHPASANAGDRLOHSPPHIPGSHHEIKEEPVGSTSK
ATAAHADRUSELAQEDDDSERPQOLLOGUARBRENPOPPKIGVATPISERFORLTAV
AESVLEGTDTTGOLFRODDSERVOLARBENPOPPKIGVATPISERFORLTAV
GKDTOTTGOLFRODDSERVENSCHANNESORGATTLONGKLOLAPDRPALNTLIKGTT
GKDTOHYLAHHASDGSQHLLLDNKGHLFDIKSTAYTSVSULNSHPGEIKGKLAQAGT
GSSVSUCOKSKATSLGSGTQSHNKTMLSQPGEAHRSLLYGINGHPAGARPQGESIRLH
DDKIHLHPPELGVWGADKDTHPGOLSRQADGSTAALKDNRTLONLSDNKSSEKLUDKI
KSYSVDQRGQVAILTDTPGRHKMSIMPSLDASPESHISLSLHFADAHQGLLHGKSELE
                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mSILTLNNNTSSSPGLFQSGGDNGLGGHNANSALGQQPIDRQTI
EQMAQLLAELLKSLLSPQSGNAATGAGGNDQTTGVGNAGGLNGRKGTAGTTPQSDSQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITVKPNSAGKKSHVEITNSSFEHASDKILQLNADTNLSVDNVKAKDFGTFVRTNGGQQ
GNWDLNLSHISAEDGKFSFVKSDSEGLNVNTSDISLGDVENHYKVPMSANLKVAE"
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KGATLRDLLARDDGETQHEAAAPDAARLTRSGGVKRRNMDDMAGRPWVKGGSGEDKVP
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SKLTFSVDTSANLDLRAGINLNEDGSKPNGVTARVSAGLSASANLAAGSRERSTTSGQ
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REQTEKAILDGKVGREEVGVLFQDRNNLRVKSVSVSQSVSKSEGFNTPALLLGTSNSA
AMSMERNIGTINFKYGQDQNTPRRFTLEGGIAQANPQVASALTDLKKEGLEMKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'translation="MELKSLGTEHKAAVHTAAHNPVGHGVALQQGSSSSSPQNAAASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3146. .8662
/gene="dspA"
/function="involved in pathogenicity"
                         /lab_host="pear and apple trees"
complement(1605, 3035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="DspA protein"
/protein_id="CAA74156.1"
/db_xref="G1:2695858"
/db_xref="SPTREMBL:054581"
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                                                                                                                                                                                                    /codon_start=1
transl_table=11
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/db_xref="GI:3150150"
                                                                                                                                   complement(1605. .2948)
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="hrpw"
3076. .3101
/gene="dspA"
3076. .8662
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/gene="dspB"
8675. .9143
/gene="dspB"
8724. .9143
/gene="dspB"
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/gene="dspA"
                                                                                                      /gene="hrpW"
                                                                                                                                                                       /gene="hrpW
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/product="potential ORFB-specific chaperone"
/protein_id="aAF63399.1"
/protein_id="AAF63399.1"
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/protein_id="aAF63399.1"
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SSYDEASFVSACVQMIEVAKRWQGKFLHGRALPTAAPRMLAQPGLTLNLAGKIK"
936. 941.
948. .2129
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AGGSPPVTDHPDPVGSAGIGAGNSVAFTSAGANQTVLHDTITVKASQVFDGKGQTFTA
GSELGBGGGSENQKPLFILEDGASLKNYTMGDDGADGTHLYGDAKIDNLHYTNVGEDA
ITVRPNSAGKKSHVEITNSSFEHASDKILQLNADTNLSVDNVKAKDFGTFVTNGGQ
GNWDLNLSHISAEDGRESFVKEDSEGLKVNTSDISLSDVENHYKVPMSANLKVAE"
complement(2587. .2592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MNISGLRGGYKSQAQQADNASSSSTGGSPAPTGRRLQRQDALPA
NYKYHASQADPATPERARVARYARASASSAGSELLGRQGARENPSLYRHEFWQQS
NYKSHGDPLPEKPETYPKRLQEKIDSYNLPRLNKLDKNLYEYGKMATELAKESGSSSY
ALMRANGKVLPLLADAENARNPGLNLHVYKRGEECYQAIKEQHKIVQOSGQPKTWRAL
                                                                                                                                               /translation="GTGIGMKAGIQALNDIGTHSDSSTRSFVNKGDRAMAKEIGQFMD
QYPEVFGKPQYQKGPGQEVKTDDKSWAKALSKPDDDGWTPASWEQFNKAKGMIKSAMA
GDTGNGNLQARGAGGSSLGIDAMMAGDAINNWALGKLGAA"
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RIQNSEWDCIMYSLMNALKSFKHHDEYTARLHKGEKIPVPAEFFKHAQSKSMVEGLPH
QDAIVTKDKGGLHAETLLHRNLAYRADRFDHACNTSIEGFRMQEIQRAGEFLSAQNRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MMMKSAEIPPAESWVDVVNSQQRLSPEQYQAFQRAISQVKORLQ
QVLGRPMPQRQGEFELDSFVDSLHADFLNVDGKAANDDVGQTAWWITRYLADRLLELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mSILTLNSNTSSSPGLFQSGGDNGLGGHNANSALGQQPIDRQTI
EQMAQLLAELLKSLLSPQSGNAATGAGGNDQTTGVGNAGGLNGRKGTAGTTPQSDSQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLSEMGNNGLDQAITPDGQGGGQIGDNPLLKAMLKLIARMMDGQSDQFGQPGTGNSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORFB; similar to ORFB of Erwinia amylovora Ea321,
AvrRxv of Xanthomonas campestris pv. vesicatoria, AvrA of
Salmonella enterica, and YopJ of Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"virulence/avirulence effector protein homolog"
/protein_id="AAF63400.1"
/db_xref="GI:7542325"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ដ
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                                                                                                                                                                                                                                                                     chaperones and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"probable Hrpw-specific chaperone"
/protein_id-"AAF63401.1"
/db_xref-"GI:7542326"
                                                                                                                                                                                                                                                                     /note="ORFA; member of SycH family of chaperone-like proteins; leucine-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="hrpw"
complement(2579. .3922)
/gene="hrpw"
/note="Hrpw family harpin;
/note="HrpN family harpin"
                                                                   /product-"harpin HrpN"
/protein_id-"AAF63398.1"
/db_xref-"GI:7542323"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 class III pectate lyases /codon_start=1.
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/protein_id-"AAF63402:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2145. .2184
complement(2253. .2582)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2579. .3934)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pseudotuberculosis"
                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
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/transl_table=11
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                                                  l_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"ORFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLECORG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          terminator
CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF083620 4291 bp DNA BCT 12-APR-2000 Erwinia amylovora harpin HrpN (hrpN) gene, partial cds. potential ORPB-specific chaperone, virulence/avirulence effector protein homolog, probable HrpW-specific chaperone, and harpin HrpW genes, complete cds; and Hrp-secreted pathogenicity/avirulence protein DSPE (dSpE) gene, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Erwinia amylovora
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1749
                                                                                                                                                                                                                                                                                                                                                                                                                aaaatagacaatctgcacgtcaccaacgtgggtgaggacgcgattaccgttaagccaaac 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1201 catatcagcgcagaagacggtaagttctcgttcgttaaaagcgatagcgaggggctaaac 1260
                                                                                                                                                 1808 TITGGTACTITIGTACGCACTAACGGCGGTCAACAGGGGTAACTGGGATCTGAATCTGAGC
                              ggcgatggcggccagtctgaaaaccagaaaccgctgtttatactggaagacggtgccagc
                                                    2108 GGCGATGGCGGCCAGTCTGAAAACCAGAAAACGCTGTTTATACTGGAAGACGGTGCCAGC
                                                                                                                                                                                                                                                                     AAAATAGACAATCTGCACGTCACCAACGTGGGTGAGGACGCGGATTACCGTTAAGCCAAAC
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Kim,J.F., Zumoff,C.H. and Beer,S.V.
Direct Submission
Submitted (12-AUG-1998) Plant Pathology, Cc
Plant Science Bldg., Ithaca, NY 14853, USA
Location/Qualifiers
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Kim,J.F., Laby,R.J. and Beer,S.V.
Comparison of the hrbN flanking regions
strains with different host specificity
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2 (bases 1 to 8143)
Bogdanove, A.J., Klm, J.F., Wel, Z.-M., Kolchinsky, P. and Beer, S.V.
Briect Submission
Submitted (07-APR-1997) Plant Pathology, Cornell University, 334
Plant Science Bldg., Ithaca, NY 14853, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bogdanove, A.J., Kim, J.F., Wel, Z., Kolchinsky, P., Charkowski, A.O., Conlin, A. K., Collmer, A. and Beer, S.V.
Homology and functional similarity of an hrp-linked pathogenicity locus, dspEF, of erwinal amylovora and the avirulence locus avrE pseudomonas syringae pathovar tomato
Proc. Natl. Acad. Sci. U.S.A. 95 (3), 1325-1330 (1998)
                                                                                                                                                                                                     961 aaaatagacaatctgcacgtcaccaacgtgggtgaggacgcgattaccgttaagccaaac 1020
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     GGCAGCACGCCGGTAACCGATCATCCTGACCCTGTTGGTAGCGCGGGCATCGGGGCCGGA 3203
                          ctgaaaaacgtcaccatgggcgacgacggggcggatggtattcatctttacggtgatgcc
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Erwinia amylovora HrpW (hrpW) gene, I
operon, complete sequence; and lysR I
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/db_xref="GI:7542328"
/translation="MELKSLGTEHKAAVHTAAHNPVGHGVALQQGSSSSSPQNAAASL
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                                                                                                                                                /product-"Hrp-secreted pathogenicity/avirulence
                                                                                                                 syringae"
                                                                                                                                                                                                                                                              Length 4291;
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3980. .4005
/note="HPDL-dependent promoter consensus; hrg
4050. .4000
/note="HPDL-dependent promoter consensus; hrg
4105. .>4291
/gene="dapE"
4105. .4110
/gene="dapE"
/qene="dapE"
/qene="dapE"
/note="similar to AvrE of Pseudomonas syringe
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Pred. No. 0;
0; Mismatches
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/transl_table=11
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1140

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pathogenicity e locus avrE

03-MAR-1998 cds; disease specific gene, partial cds.

us-09-596-958-1.rge

source

gene

CDS

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/protein_id="AACO4851.1"
//protein_id="AACO4851.1"
//d_xxef="cd::2668589"
//translation="WINSOQORVERFLOYFSACCKTPIHLKDGVCALYNEQDEEAAVLE
VPOHSDSLLLHCRITEADPOTSITLYSMLLOINFEMAAMRGCWLALDELHNVRLCFOO
SIGHIDEASFSDIVSGFIEHAAEVREYIAQLDESSAA"
//note="partial ORF"
                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MFISKSMQVFITLYQEKSLKTAADKLCLTVPPVSRMLKLTEGWV
GEQLETIERNNITPTFAADCIYQQLLPLYMALKNWTRKHPEQQEFLIASPYISTSILS
DLLTISESALPKCSSIKYAECHPDDDIYISLQPVECPWHFEPTRMDLYLELCCSKDV
GDKWLHMPILAESETKYTYGVELAELHARGGSGVLRQVDNPSHLQSTFKSGEGLLF
RLPPRNNWXDYQESTKKLTSTRELHARGGSGVLRQVDNPSHLQSTFKSGEGLLF
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Pseudomonas syringae hrp type III secreted protein (hrpW) gene,
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1 (bases 1 to 1833)
Charkowski,A.O., Alfano,J.R., Preston,G., Yuan,J., He,S.Y. and
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Pseudomonas syringae pv. syringae
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VERSION
KEYWORDS
SOURCE
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MLSEMGNNGLDQAITPDGQGGGGIGDNPLLKAMLKL"
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SEVLEGTDTTOSPLKPOSMKGSGACYPLATTDKGKLGLABDNPPALNTLLKGTL
GKDTOHRLAHHASSOROSQULLLDNKGHLFDTKSTATSYSVLHNSPGEIKGKLAQAGT
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KSYSVDORGOVALIDTPGRRHKMSIMPSLDASPESHISLLGISLHRANSEKLVDKI
KSYSVDORGOVALIDTPGRRHKMSIMPSLDASPESHISLSLHFBAHOGLLHGKSELE
AGSVAISHGRLVVADSEGKLFSAAIPKQGGGNELKMKAMPQHALDEHFGHDHQISGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDDHQQLNALVKNNFRQQHACPLGNBHQFHPCWNLTPALVIDNQLGLHHTNPEFHEIL
DMGHLGSLALQFGKLHYFDQLTKGWTGAESDCKQLKKGLDGAAYLLKDGEVKRLNINQ
STSSIKHGTENVFSLHYRNKPEPGALQGLKKDDKAQAMATGVNKYLALTEKGBIR
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AESSSWHKLALDVSEKIKSLDMSHBHKPIATFEDGSQHQLKAGGWHAYAAPERGPLA
VGTSGSQTVFNRLMQGVKGKVIPGSGLTVKLSAQTGGWTGAEGRRVSSKFSERIRAYA
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KGATLRDLLARDDGETQHEAAAPDAARLTRSGGVKRRNMDDMAGRPMVKGGSGEDKVP
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KELTULGEBRGAELLNDMKRRRDELGSATRSYTVLGQHQGVLKSNGEINSEKRSPG
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GRQRDPNDKTALTKSRLILDTVTIGELHELADKAKLVSDHKPDADQIKQLRQDFOTLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKRYESNPVKHYTDMGFTHNKALEANYDAVKAFINAFKKEHHGVNLTTRTVLESGGSA
ELAKKLKNTLLSLDSGESMSFSRSYGGGVSTVFVPTLSKKVPVPVIPGAGITLDRAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSFSRTSGGLNVSFGRDGGVSGNIMVATGHDVMPYMTGKKTSAGNASDWLSAKHKISP
DLRIGAAVSGTLQGTLQNSLKFKLTEDELPGFIHGLTHGTLTPAELLQKGIEHQMKQG
SKLTFSVDTSANLDLRAGINLNEDGSKPNGVTARVSAGLSASANLAAGSRERSTTSGQ
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DGIVELLHKHFDAALPASSAKRLGEMMNNDPALKDIIKQLQSTPFSSASVSMELKDGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MELKSLGTEHKAAVHTAAHNPVGHGVALQQGSSSSSPQNAAASL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQQKRHQLNNFGQMRQTMLSKMAHPASANAGDRLQHSPPHIPGSHHEIKEEPVGSTSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sedneuce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="hrpL-dependent promoter consensus sequence,
box,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="disease specific operon"
/note="hrpL-dependent promoter consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542. .6609
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542. .6128
/gene-"dspE"
612. .6128
/gene-"dspE"
                                                                                          /note="disease specific operon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAC04850.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(473. .501)
                                                                                                                 complement(<1. .501)
                                                                  /db_xref-"taxon:552"
                                                                                                                                                                  complement(<1. .414)
                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                     /note="harpin"
                                                                                                                                          /gene="hrpW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="hrpW"
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/no+
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8

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ALLEDTARQKDVSFGQPDNTVQNPTDSSAJDPGSNLSGKSPQTNTFSDESTAGGVDP
SALLEDTARQKDVSFGQPDNTVQNPTDSSAATDPQSNVVKLLSALVTSLLQMLMNLNK
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HQKPLFELAEGAVLKNVNLGENEADGIHVNAKNSEQVTIDNVHAQNVGEDMITVKGGG
GAKVTNLNITNSSANGADDKVIQLNADTHLKVDGFKATDFGTLVRTNGGKQFDDMSVE
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                                                                                                                  Charkowski,A.O. and Collmer,A.
Charkowski,A.O. and Collmer,A.
Direct Submission
Submitted (10-DEC-1997) Plant Pathology, Cornell University, Plant
Science Bldg. Rm 334, Ithaca, NY 14853, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1054 TTTACCGCCGACAAGTCGATGGGCACCGGCGACCAGCACAACATCAGAAGCCCCTGTTC 1113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             994 GTCGTGAAAGACACCATCAAAGTCGGTGCTGGCCAGGTGTTTGACGGCCACGGTGCAACC 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgggtgaggacgcgattaccgttaagccaaacagcgcgggcaaaaatcccacgttgaa 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1048 atcactaacagttccttcgagcacgcctctgacaagatcctgcagctgaatgccgatact 1107
Collmer, A.
The Pseudomonas syringae pv. tomato HrpW protein has domains similar to harpins and pectate lyases and can elicit the plant hypersensitive response and bind to pectate
J. Bacteriol. 180 (19), 5211-5217 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   820 ttcaccgccggttcagaattaggcgatggccagtctgaaaaccagaaaccgctgttt 879
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Pred. No. 1.9e-34;
0; Mismatches 225; Indels 15;
                                                                                                                                                                                                                                            1. 1833
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/function="pectate binding"
/note="HrpW; harpin"
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                                                                                                                                                                                                                                                                                  /strain="B728a"
/db_xref="taxon:321"
/note="pathovar syringae"
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                                                                                                                                                                                                                                                                                                                                                                                                                              /note="hrp box"
268. 1593
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/gene="hrpW"
115. .139
/gene="hrpW"
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59.1%;
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/gene="hrpW"
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Best Local Similarity 59.1
Matches 347; Conservative
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    J. Bacter
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                                                                                                                                           AUTHORS
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                                                                                                   MEDLINE
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                                                                              JOURNAL
                                                                                                                                                                                                                         FEATURES
                     TITLE
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1225 ttctcgttcgttcaaaagcgatagcgaggggctaaacgtcaataccagtgatatctcactg 1284
                                                              ggtcaacag---ggtaactgggatctgaatctgagccatatcagcgcagaagacggtaag 1224
                                                                                            1414 GCCAAGCAGTTTGATGACATGAGTTCGAGCTCAATGGCGTGGACGCGACCCATGGCAAG 1473
                                                                                                                                                            1474 TTCGCACTCGTCAAAAGCGACAGTGACGATCTGAAACTGGCCACTGGCGACATCGCCATG 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Pseudomonas syringae pv. tomato HrpW protein has domains similar to harpins and pectate lyases and can elicit the plant hypersensitive response and bind to pectate

Bacteriol. 180 (19), 5211-5217 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charkowski, A.O., Alfano, J.R., Preston, G., Yuan, J., He, S.Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Direct Submission
Submitted (23-MA-1997) Plant Pathology, Cornell University, Ithaca, NY 14853, USA
                                                                                                                                                                                                                                                                                                            AF005221 1729 bp DNA BCT 05-OCT-19
Pseudomonas syringae hrp-secreted protein HrpW (hrpW) gene,
                                                                                                                                                                                                               1534 ACCGACGTCAAGCACGCCTATGACAAGACCAAGGCGTCTACCCAGCA 1580
                                                                                                                                                                                              1285 ggtgatgttgaaaaccactacaaagtgccgatgtccgccaacctgaa 1331
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268. 1693
/gene="hrpw"
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/organism="Pseudomonas syringae"
/strain="DC3000"
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/transl_table=11
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/gene="hrpW"
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/gene="hrpW"
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protein has domains similar to
the plant hypersensitive response
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GTVGRAIEANRRRGLPVDYWNLNLPRETQDYVPRLLALSMYVRNDNAYGVKLTPVANTP
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                                                                                                                                                     "The Pseudomonas syringae Hrp pathogenicity island has a tripartite mosaic structure composed of a cluster of type III secretion genes bounded by exchangeable effector and conserved effector loci that contribute to parasitic fitness and pathogenicity in plants; Proc. Natl. Acad. Sci. U.S.A. 97(9):4856-4861(2000).
                                                                                              MEDLINE; 20243785.
URMED: 10781092.
Alfano J.R., Charkowski A.O., Deng W.L., Badel J.L., Petnicki-Ocwieja T., van Dijk K., Collmer A.;
                                                                                                                                                                                                                                                                                              2000) to the EMBL/GenBank/DDBJ databases.
UNLV, 1854 Maryland Parkway, Las Vegas, NV 89154, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="conserved effector locus flanking the hrp/hrc
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"The Pseudomonas syringae pv. tomato HrpW harpins and pectate lyases and can elicit and blud to pectate";
J. Bacteriol. 180(19):5211-5217(1998).
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complement(1082. .2569)
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                                                                                    Gaps
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                                                                                   15;
                                                      Length 1729;
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                                                      Score 155.2; DB 1;
Pred. No. 6.9e-29;
0; Mismatches 233;
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Bacteria; Proteobacteria; gamma
Pseudomonas syringae.
                                                      Query Match 11.5%;
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ODALTQVAPSARPPTKKLGTGTKHQGTKLSHQKADD FLGGFKDASEDHGLEKRARLADL
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VMTTPPFILLADKATGLMPTAGATGNYT ILLBGARGNSGGFRAG
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VDDLFFEGGLNNPLQVLKKAVDHESYEARRFNFDLTAGGTADIRAGINLTEDRDPNADPNS
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NVVSDLVTARNTVGGWKGAGPIVAAAVPQFLSSMTHLGYVRLSTSDKLRDTIPETSSDA
NMLKASIIGWVAGIAHETVNSVVKPMFQAALQKTGLNERLNMVPWKAVDTNTVIPDPFE
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EGDDPKLKLMPEQANFQLEGVPLGGHNRVTGFINGDDGGVHALIKNRQGFTHSHALDEQ
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FGRSGVEKSKKASTSEFIRANIYKNTAETPRWKNVGDHIQHRYQGRLGLKEVYETESM
LFKQLELIHESGGRPPARGQDLKARITALEAKLGPQGATLVKELETLRDELENHSYTAL
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OMLNDVHQINGQTLSARALASGFGGAVSASSQTLLOLKSNYVDPQGRKIPVFTPDRAES
DLKKDLLKGMDLREPSVRTTFYSKALSGIQSSALTSALPPVTAQABGASGTLSAGAILR
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KEIEGLDDRVIKAFAMYSNKRFVALDDQNKLTAHSKDHKPVTLDIPGLEGDIKSLSLDE
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ASAPGNATRVAEFMRQDPKLRAMLKEMEGSIGTLARVRLEPKDSLVDKIDEGSLNGTWT
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                                                                                                                                                      SSKLQSGWNLTNALVLNNNRGLTMPPPPTAADRLNLDRAGLVGLSEGRIQRWDATPECW
                                                                                                                                                                                                                                                                                      KHNLHALTSTGGLYCLPKEAWQSTKLGDQLRARWTPVALPGGQPVKALFTNDDNVLSAQ
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Pred. No. 6.4e-29;
); Mismatches 233;
                                                                                                                                                                                                                                                                                                                                                                                     QRPAREADIEEGGTAASPSEIPFRPMRS
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57.1%;
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YQTVYAQRAGAVAAPTAGLHFDOPLMEAIAAKGVETAFVTLHVGAGTFQPVRVEQIED
HHMEBWLESGDVVDAVVAACRARGGRVIAVGTTSVRELESAARDGOLKPFSGDTDIF
IYPGRPFHVVDALLYMPHLLPESTLLMLVSAFAGYPETWAAYAAAIEHGYRFFSYGDAM
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Plant Sciences Bldg., Ithaca, NY 14850, USA
Sequence update by submitter
On Mar 14, 2001 this sequence version replaced g1:3228544 g1:790906
gi:3228541 gi:807790 gi:11776506.
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complement(2908. .3324)
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                                                                                                                                                                                                                /note="exchangeable effector locus flanking the hrp/hrc
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                                                                                                                                                                                                                                                                                                           /gene="queA"
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                                                     COMMENT
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Alfano,J.R., Charkwaski.A.O., Deng.W.L., Badel,J.L.,
Petnicki-Ocwieja,T., van Dijk,K. and Collmer,A.
The Pseudomonas syringae Hrp pathogenicity island has a tripartite mosaic structure composed of a cluster of type III secretion genes bounded by exchangeable effector and conserved effector loci that contribute to parasitic fitness and pathogenicity in plants
Proc. Natl. Acad. Sci. U.S.A. 97 (9), 4856-4861 (2000)
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Deng, W.L., Preston, G., Collmer, A., Chang, C.J. and Huang, H.C.

Characterization of the hrpc and hrpRs operons of Pseudomonas
syringae pathovars syringae, tomato, and glycinea and analysis of
the ability of hrpf, hrpG, hrcC, hrpT, and hrpV mutants to elicit
the hypersensitive response and disease in plants
J. Bacteriol. 180 (17), 4523-4531 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                   Preston,G., Huang,H.C., He,S.Y. and Collmer,A.
The HrpZ proteins of Pseudomonas syringae pvs. syringae, glycinea,
and tomato are encoded by an operon containing Yersinia ysc
homologs and elicit the hypersensitive response in tomato but not
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                                                                                                                                                                                       pathogenicity
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The Pseudomonas syringae pv. tomato Hrpw protein has domains similar to harpins and pectate lyases and can elicit the plant hypersensitive response and bind to pectate by Bacteriol. 180 (19), 5211-5217 (1998)
                                                                                                                                                                                                                                                                                                                                 Pseudomonas syringae pv. tomato
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Charkowski,A.O., Alfano,J.R., Preston,G., Yuan,J., He,S.Y. and
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Ramos,A.R., Rehm,A.H. and Collmer,A.R.
Pseudomonas syringae pv. tomato DC3000 hrpL through hrcU
                                                                                                                                                          AF232004 52498 bp DNA BCT
Pseudomonas syringae pv. tomato strain DC3000 Hrp
18land, complete sequence.
AF232004 AF061028 AF051029 AF232006 L41861
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Alfano, J.R. and Collmer, A.
Direct Submission
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TSSKRELINNMKSLKASGVTTLFMEHLCAEGHDKALNNYLSAFKGSPMPARLKNYLDL
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3 (bases 1 to 1245)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L (sites)
Hatada,Y., Saito,K., Koike,K., Yoshimatsu,T., Ozawa,T.,
Kobayashi,T. and Ito,S.
Deduced amino-acid sequence and possible catalytic residues
novel pectate lysse from an alkaliphilic strain of Bacillus
Eur. J. Blochem. 267 (8), 2268-2275 (2000)
cagaaaccgctgtttatactggaagacggtgccagcctgaaaaacgtcaccatgggcgac
                                                                                   gacggggcggatggtattcatctttacg-----gtgatgccaaaatagacaat
                                                                                                                                                                           973 ctgcacgtcaccaacgtgggtgaggacgcgattaccgttaagccaaacagcgcgggcaaa
                                                                                                                                                                                                                                                                   1033 aaatcccacgttgaaatcactaacagttccttcgagcacgcctctgacaagatcctgcag
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Bacillus sp. gene for pectate lyase, complete cds.
ABO11839
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/evidence=experimental
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2223. .2582
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2244. .2582
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71. .77
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Lazarevic, V.
                                                                                                                                                                                                                                                                                                                                                                                  /gene="prfB"
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DGKGGTYVANPWTLGDGSDRNQKPIFRLEAGASLKNVVIGAPAADGVHCYGDCTITN
VIWEDVGEDALTLKSGGTVNISGGAAYKAYDKYPQINAGTINIRNFRADDIGKLYRO
NGGTTYKVVMNVENCNISRVKDAILRTDSSTSTGRIVNTRYSNVPTLFKGFKSGNTTA
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1 (bases 1 to 47739)
Reizer,J., Hoischen,C., Titgemeyer,F., Rivolta,C., Rabus,R., Stulke,J., Karamata,D., Saler,M.H. Jr. and Hillen,W.
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Robinson,C., Rivolta,C., Karamata,D. and Moir,A.
The product of the yvoC (gerF) gene of Bacillus subtilis is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        672 TGGGAGGATGTTGGTGAGGATGCGCTGACGCTTAAATCGTCCGGAACG------
                                                                                                                                                                                                                             18;
                                                                                                                                                                                           Length 1245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF017113 47739 bp DNA BCT
Bacillus subtilis 300-304 degree genomic sequence.
AF017113
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Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                             0; Mismatches 224;
                                                                                                                                                                                          Score 95.6; DB 1;
Pred. No. 1.1e-13;
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98230327
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protein: PIR Accession Number \$43727 and to Bacillus subtilis YqfU, YpjC and YltB proteins"

/ccdon_start=1 TETERATE TO THE WELSE TRABLENMASKLADFRGSLDLESKEARTAELDEGMADPE FWNDQOKAQTVINEANGLKDYVNSYKKLNESHEELOMTHDLLKEEPDTDLQLELEKEL KSLTKERNEFELQLLLSEPYDKNNAILELHPGAGGTESQDMSGMLLAWTRWGERRGF KYTLDYLEGDEGGIKSVTLIKGHNEYGYKKARKGYHRLVRISPSGKRHTSFVS CVEWMPERDENDETDIDTRYBTRYDTYRAGGAGGOHVNTYDSAVRITHLEPHNVYYTCQTE RSQIKNRERAMKMLKAKLYQRRIEEQQAELDEIRGEGKEIGWGSQIRSYVFHPYSWVK ISTILQSYGFEAAYVQWIINIPLFIAGVILLGGKFGLKTLAGSVFLPLVVFLTRDIQP ATHHELLAA FIGWCIGIGOTYLLGKGSTGGTAAQIIHKYSGLSLGKCLAIIDGM IVVTAMIVENIEQGLYAMLGVYSSKTIDVVQVGFRARALIITKGEQAVKENVLQK IDRGVTKISAVGGTPPDDRPILMCVVGQTEFTKLKQIVKQIDESAFVIVADASEVLGE /protein_1d="AAC67260.1" /db_xref="G1:2618831" /translation="MDVRNKTLWILRDYVYILIGAAITAVSFNVFLLPNKIAAGGVSG /note-"at low concentrations of RF-2 nucleotides 155. .15: (UGAC) are translated as Asp, Pel,H.J. Nucleic Acids Res. 20, 4423-4428, 1992" /codon_start=1 Nucleotide sequence of the 300-304 chromosomal segment of Bacillus /product="putative peptide chain release factor RF-2" /protein_id="AAC67303.1" /db_xref="GI:2618874" 3 (bases 1 to 47739) Lazarevic, V., Soldo, B., Rivolta, C., Reynolds, S., Mauel, C. and Direct Submission Submitted (05-AUG-1997) IGBM, Cesar-Roux 19, Lausanne 1005, DHRTNTEMGNVQAVMDGDIDTFIDAYLRSKLS" required for spore germination Microbiology 144 (Pt 11), 3105-3109 (1998) 99061203 1. .47739 /Organism="Bacillus subtilis" /db_xref="taxon:1423" /map="300-304 degrees" /note="putative lipoprotein" join(83. .154,156. .1184) /gene="prf8"

gene

CDS

gene

RBS

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ANLIFILLSSSHSVLFIMIGILGGLASGVGLTSMIGHTSMIAMICT
RIFGGLISSALIGGLASGTHTLEMILFAVSTIGVFVSLGIKSDETARIEKNSA"
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HFLWIPYFVGFGQRVQGSLPETSIRITAKRVCILGLAVAVLGAASLLWTPLAGAAVCT
                                                       ALLGRIFLSIKQRVNDNAAPFYFSKRDQGLMVLGIIPNTPAEDLELKIGEIITKVNGI
PVKNVSDFYEALQHNRAYVKLEIIGLNGEIRFDQRASYEGEHHELGILFVKDDREDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="belongs to the TetR/AcrR family of transcriptional regulators"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37582 AAAGGACAGCGGTTTGTGGCAGGGAAAGAATTAGGTGACGGAAGCCAGTCAGAAAACCAA 37523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37642 GCAGCTGACAAAGTGGTGCACGAAACAATTATCGTACCAAAAAATACAACATATGACGGG 37583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGCTGATGGCGTGCACACTTATGGAAACGTTAACATTCAGAATGTGAAATGGGAAGAT 37403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       748 gctaatcagacggtgctgcatgacaccattaccgtgaaagcgggtcaggtgtttgatggc 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ggggcggatggtattcatctttacggtgatgccaaaatagacaatctgcacgtcaccaac
                                                                                                                                                                                                                         /note="belongs to the major facilitator family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 47739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91; DB 1; 1
Pred. No. 1.4e-12;
                                                                                                                                                                     complement(8025. .9359)
/gene="yvkA"
                                                                                                                             complement(8025. .9373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(9366. .9373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(9390. .9972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(9390. .9959)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        988 gtgggtgaggacgcgattaccgttaag 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="YvkB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="yvkA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="9959"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="yvkB"
                                                                                                                                                        /gene="yvkA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:2635827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
Bacillus subtilis
                                                                                                      VASGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z99121 AL009126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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to 3609060.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BSUB0018
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Matches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
BSUB0018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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VIAKWLSEKK"

YOGONE-1613
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ADEPTGNLDPDTSWRVMTLLEEINNRGTTVVMATHNREIVNTMKKRVTAIEDGIIUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mikilgrhlresfkslgrntwmpfasisavtvtllugvpluim
LNLNNmatnaerqveikvlidltadgkaqdklgndikelkgigsvtfsskekeldglv
DSFGDSGKSLTmkDQEnpLnDafvvkTtDPHDTPnVakkiekmDHVykVTyGkeevSR
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ISTFSEHTAEDFAKALRELEKKEIEGLVIDVRGNPGGYLQSVEEILKHFVTKDQPYIO
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KVDMNNEDVKHAQVLLKGLSFDPGREDGYFSKDMKRAVMAFQDQNKLNKTGVIDTRTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFKVVGVSRNIGIALIIGIVFTAMFLISNTIKITIFARKEIEIMKLVGATNWFIRWP
FFLEGLLLGVFGSVIPIALVLSTYQYVIGWVPKVQGSFVSLLPYNPFVFQVSLVLIA
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4512. .5967

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/gene="yvjB"

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/transl_table=11

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/protein_id="AAC67263.1"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="YvjD"
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3495. .4385

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6773. .6777
/gene="yvjb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3476. .4385
/gene="ftsx"
3476. .3484
                                                                                                                                                                                                                    2816. .3502
/gene="ftsE"
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/gene="yvjD"
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gene

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LLTGTLPARKGRVYLAGKLLADYRPRELAQIMAVLPOKMOQAFTFTVEETVAFGRYPF
VGCLFRQOTREKGALYVDEAMEDGYVADAGKRIPRELSGGEOGRYVLAGAAQOPRILE
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SMSVSTLILTGVITNSFLGAFISLIALTGDNLLPITHWLLGSVSMRGWSYVILEPPR
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DEBRWYQFFEVRWASAVRTSRHELPKMLAKNSGRILAINASAGSGYKPLPTWAIPYSWTYA
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EPTSLIQRYATAEEVANTIVFLASDAASAINGTAQRVEGGIIRSL
                                                                                                                                                                                                                                                   DDILLQTEIPLRTLSSTPIGAGFSWSRTLIHKRLPDOPDPIEGLTÄCLSESGFOLGET
TRAMSSERIDDRVYRTYEDEDELSVFICVQTGFSIWILINGYAADOFFIKALMAAEAER
TRVLGDGGGTGDILIAATOTQQSENIEORLNQLIKKGTAECIKEAAELFE"
complement(1977. .3038)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLLGTILLIINGRELNVMTYGEDKAKLLGVSVQQRKMMILIAGSLLTGSAVAVSGTIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MDLQLKEKLVLITGSTSGIGKAAAKSFLQEGAAVIVNGRKQETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4343. .5165
/gene="yvrb"
4343. .5134
4343. .5134
/gene="yvrb"
/function="unknown"
/note="similar to ketoacyl-carrier protein reductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"similar to iron-binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to RNA polymerase"
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complement(3001. .3945)
                                                                                                                                                                                                                                                                                                                                                                                                         complement(1977. .3038)
/gene="yvrB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3001. .3945)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function-"unknown"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="yvrE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="yvrc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5145. .5165
/gene="yvrD"
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                Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Baredo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Bortis, R., Boussier, B., Sanas, A., Brann, M., Brigotal, S.C., Bortis, S. Bruschi, C. V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J. J., Connerton, I.F., Cummings, N. J., Carter, N.M., Choi, S.K., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P. Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galler, C., Fulima, K.D., Galizzi, A., Galler, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galler, C., Fujita, M., Fujita, Y., Halech, J., Harwood, C.R., Henaut, A., Hibett, H. Holasppel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kashara, Y., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koningstein, G., Krogh, S., Kananato, D., Kashara, Y., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Andigus, A., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauell, C., Medigue, C., Media, N., Mellado, R.D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Portelle, B., Rapoport, G., Roche, B., Rose, M., Sadaie, Y., Sato, T., Sekowska, A., Seror, E., Takahashi, H., Takamaru, K., Takeuchi, M., Tamakoshi, A., Tanakoshi, A., Tanakoshi, A., Tanakoshi, A., Tanakoshi, A., Tanakoshi, A., Yamamoto, H., Yamamoto, K., Yasumoto, H., Ander, M., Yasumoto, K., Y
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Direct Submission
Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,
Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
addanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
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EAPELKKFILPGGSKCASLLHIARTITRRAERRVVALMKSEEIHETVLRYLNRLSDYF
FAGARVVNARSGIGDVEYERRAIVFRDRNSSES"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
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/codon_start=1
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/gene="yvqK"
complement(4. .29)
/gene="yvqK"
complement(45. .626)
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                                   AJ237980.1 GI:4585731
pectate lyase; pelA gene.
Bacillus sp. BP-23.
Bacillus sp. BP-23.
Bacillus Sp. BP-23.
Bacillus Strain aroup:
Bacillus Staphylococcus group; Bacillus.
1 (bases 1 to 1214)
Soriano,M., Blanco,A., Diaz,P. and Pastor,F.I.
An unusual pectate lyase from a Bacillus sp. with high activity of pectin: cloning and characterization
Microbiology 146 (Pt 1), 89-95 (2000)
                                                                                                                                                                                                                                                                                                                                                               Submitted (12-APR-1999) Pastor F.I.J., Microbiology, Faculty of Biology, University of Barcelona, Av. Diagonal 645, 08028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        742 gccggcgctaatcagacggtgctgcatgacaccattaccgtgaaagcgggtcaggtgttt 801
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Bacillus sp. pelA gene for pectate lyase, strain BP-23 AJ237980
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/function="pectate degradation"
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272 c 306 g 307
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39. .44
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/gene="pelA"
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ilarity 51.9%;
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/gene="r
62
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95
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KOPPGRAMAGATTSMBEESQKQASLYRLNDGSLYKIKDQVSTSNGLDMPRERNLAXYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to two-component response regulator [YvrG]"
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                                                                                                                                                                                                                                                                             'note="similar to two-component sensor histidine kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aaaggacaaaccttcaccgccggttcagaattaggcgatggcggccagtctgaaaaccag 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggggcggatggtattcatctttacggtgatgccaaaatagacaatctgcacgtcaccaac 987
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58.8%; Pred. No. 1.4e-12;
ive 0; Mismatches 110; Indels
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                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
/protein_id="CAB15326.1"
/db_xref="GI:2635834"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAB15327.1"
/db_xref="G1:2635835"
                                                                                                                                                                                          /gene="yvrg"
complement(6122. .7843)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(7861. .8970)
/gene="yvrH"
                                                                                                                                                                      complement(6122. .7843)
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                                                                                                                                                                                                                                         /gene="yvrG"
/function="unknown"
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Gonzalez-Candelas, L. and Kolattukudy, P.E.
Isolation and analysis of a novel inducible pectate lyase gene from
the phytopathogenic fungus Fusarium solani f. sp. pisi (Nectria
                                                                                                                                                                                                                                                                                                                                                                                          1 (sites)
Crawford,M.S and Kolattukudy,P.E.
Pectate lyase from Fusarium solani f. sp. pisi: purification,
characterization, in vitro translation of the mRNA, and involvment
                                                                                                                                                                                                                                                                                                M94692.1 GI:168157

Pectate lysse: pectate lysse A.

Pusarium solani (individual_isolate , sub_species pisi) (library:
lambda gill) population VI cDNA to mRNA.

Fusarium solani

Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Fusarium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="the amino acid sequence of the N-terminus of the mature protein and an internal CNBr peptide have been determined"
                                                                                                                                                                                                                                       Fusarium solani pisi (Nectria hematococca) pectate lyase (pelA) M94692
                            401 TGGGAAGATGTAGGGGAGGATGCATTGACACTGAAATCATCAGGAACCGTTAATATTACC 460
           919 ggcgacgacggggggggggtattcatctttacggtgatgccaaaatagacaatctgcac 978
                                                                    979 gicaccaacgigggigaggacgcgaitaccgitaagccaaacagcgcgggcaaaaaicc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Biophys. 258, 196-205 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 884
/organism="Fusarium solani"
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/sub_species="pisi"
/db_xref="taxon:108890"
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/tissue_lib="lambda gt11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haematococca, mating population VI)
J. Bacteriol. 174, 6343-6349 (1992)
93015682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                 1039 cacgttgaaatcactaacagttcc 1062
                                                                                                                                                               461 GCCGCAGCCTATAAGCCTTAC 484
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63. 727
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/gene="pelA"
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FEATURES

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Act transporter Tarbehinding protein; ABC transporter transmembrane protein; asnC-family transcriptional regulatory protein; hydrolase; integral membrane protein; protein; hydrolase; integral membrane protein; mark-family transcriptional regulator; oxidoreductase; oxidoreductase, iron-sulphur binding subunit; oxidoreductase, molybdopterin binding subunit; regulatory protein; secreted deacetylase; secreted hyase; secreted protein; tetR-family transcriptional regulator; two component system histidine kinase; two component system response regulator; ung, uracii DNA alycosylase.

Streptomyces coelicolor.
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Cerdeno, A.M., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (113-OCT-2000) Streptomyces coelicolor sequencing project,
Sangar Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 ISA E-mail: barrell@sangar.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomyciaes; Streptomyceson 1 (bases) to 40549)
Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.
A set of crdered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome
Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 974 tgcacgtcaccaacgtgggtgaggacgcgattaccgttaagccaaacagcggggcaaaa 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1034 aatcocacgttgaaatcactaacagttccttcgagcacgcctctgacaagatcctgcagc 1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 ACATCAACGGTGGTGGTGCTTTC------CACGCCTCTGACAAGATCATTCAGT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 TCATTGGTGCTTCCCAGGCCGAGGGTGTTCACTGCAAGGGAACTTGCACTCTCAACAATG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 TCAACGCCCGCGGAACCGTCCACGTCAAGGACTTCTACGCCGAGGACTACGGAAAGCTCT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                 854 agtetgaaaaceagaaaeegetgtttataetggaagaeggtgeeageetgaaaaaegtea 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 AGACTGGTGAGAAGGATGCCATGTTCATTCTTGAGAATGGTGCCACCCTCTCCAACGTTA 252
                                                                                                                                                                                                                                                                                                                                                              12;
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Pred. No. 3.5e-05;
0; Mismatches 148;
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Streptomyces coelicolor cosmid 2G38.
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obs. .870
/gene="pelA"
884
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.• 242 c
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                                                                                                                                                                                                                                                                                                                           Similarity
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COMMENT

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// 3399. .5102
/gene="2SCG38.05"
/gene="2SCG38.05"
/gene="2SCG38.05"
/note="2SCG38.05, probable oxidoreductase, len: 567 aa;
similar to SW:AIDB_ECOLI (EMBL:L20915) Escherichia coli
oxidoreductase AldB protein, 541 aa; fasta scores: opt:
1437 z-score: 1553.6 E(): 0; 45.8% identity in 517 aa
overlap. Contains 2x pfam matches to entry PF00441
Acyl-CoA_dh, Acyl-CoA_dehydrogenase and match to Prosite
entry PSO0073 Acyl-CoA_dehydrogenases signature 2"
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[49ene="25cG38.03"
1739. 2539
[79ene="25cG38.03]
[79ene="25
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complement(12544...3350)

/gene="126G38.04c"
/gene="25GG38.04c"
/gene="25GG38.04c"
/note="25GG38.04c, conserved hypothetical protein, len:
268 aa; similar to TR:053782 (EMBL:AL021943) Mycobacterium
tuberculosis hypothetical 26.5 kDa protein MTV040.02, 240
aa; fasta scores: opt: 735 z-score: 848.5 E(): 0; 51.48
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GTHPPELPARDLYFVAGFDVGASTARAALSRWAAAGDLRRTDTGYRLSERLLERQRR
QDEALRPHTRAWDGDWETLVITATGRDPAARAELRTRLAALRLAELREGVWLRPANLD
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/db_xref="G1:10803134"
//tb_sref="G1:10803134"
/db_xref="G1:10803134"
/db_xref="G1:10803134"
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DAVREVWPDDKPLFFRVSATDWLEEGGWTPDDTVRFARDLEAHGIDLLDVSTGGNVPR
VRIPTGPGYQVPFAARVKAGSTLPVAAVGLITEPGQAEKILANGEADAVLLGRELLRN
                                                                                                                                                                                                                                                                                                                                                                     AHYGARAVGGTGLIVVEATGVSPEGRISPQDLGLMNDTQVEAFRRITGFLRSQGTVPA
VQLAHAGRKASTAQPWRGGAPVGADAYGWQPLAPSALAFDERHPVPTELTVPQIQEAV
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FAAVVRHLLADPVLPPELLPPDWPGTALRDAYARYQREQSGQVRAHGPRT"
                                                                                                                                                                                                                                                                                                                                   /translation-"MSALFEPFRLRDTTIPNRIWMPPMCQYSAAPEGPSAGVPGDWHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="2SCG38.02"
/note="Pfam match to entry PF00724 oxidored FMN,
NADH:Ilavin oxidoreductase / NADH oxidase family, score
318.10, E-value 1e-91"
1739. .2539
         PF00724 oxidored_FMN, NADH:flavin oxidoreductase / NADH
                                                                                                                                                                           /product-"putative oxidoreductase"
/protein_id-"CAC13061.1"
/db_xref-"G1:10803133"
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/protein_id="CAC13064.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSWAQHAARELGVDARMPDQYGWGM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
                                                                                                        /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prediction is based on positional base preference in codons using a specially developed Hidden Warkow Model (Krogh et al., Nucleic Acids Research, 22(2):4768-4778(1994)) and the FramePlot program of Blibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the coorect initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

    93
/note="nominal overlap with Streptomyces coelicolor cosmid
SC264"

                                                                                                                                                                                                                                                                                                                                                                                                                                                      The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Subsully the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MTPAATAAGTRELPHPTRAEIRLEGVLHALSDPVRLRIVRDLAA
DSGALFSCSHFDLPVTKSTTTYHFRVLRESGVIRQTYRGTAKMNGLRRDDLDIVFPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(41.320)
/gene="2SCG38.01c"
/note="2SCG38.01c,
possible regulatory protein(fragment),
len: >106 as; similar to N-terminal region of TR:CAC01635
(EMB:AL391072) Streptomyces coelicolor putative
regulatory protein SC944.08, 116 as; fasta scores: opt:
218 z-score: 308.8 E(): 9.3e-10; 46.2% identity in 91 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="2SCG38.02"
/note="2SCG38.02, probable oxidoreductase, len: 359 aa;
/note="2SCG38.02, probable oxidoreductase, len: 359 aa;
similar to SW:NEWA_ECOLI (EMBL:D86931) Escherichia coli
N-ethylmaleimide reductase (EC 1. -. -) NemA, 365 aa;
fasta scores: opt: 509 z-score: 564.1 E(): 5.66-24; 32.18
identity in 364 aa overlap. Contains Pfam match to entry
                                                                                                                                                                                                                                                                          (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                          reptomyces coelicolor sequencing at The Sanger Centre is funded the BBSRC and Beowulf Genomics
                                                                                                                                          by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions. Cosmid 2638.
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/protein_id-"CAC13060.1"
/db_xref-"GI:10803132"
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1. .40549

//Organism="Streptomyces coelicolor"
//db_traf="taxon:1902"
1. .40549
//organism="Streptomyces coelicolor A3(2)"
Colney, Norwich, Norfolk NR4 7UH, UK Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="A3(2)"
/db_xref="taxon:100226"
/clone="cosmid 2G38"
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/gene="2SCG38.01c"
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/transl_table=11
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sp. pisi"

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/translation="MHAPSIVTVLAALPAAMACLGYTGGVPKATGSKSLSAPKTLKKG
EVPDAGWYKTVDRGVKCSQQAEGGSKDAVFILEEGATLKNVIIGANQREGIHCKGSCNI
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RSCGNCKGNTNCKRSVHMEGTTAAVKGGELIGINTNYGDKATYSNNCYPKTQCQGYKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1104 tactaacctgagcgttgacaacgtgaaggccaaagactttggtacttttgtacgcactaa 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            State University, 1060 Carmack Road, Columbus, OH 43210, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        606 CAAGGACGCCGTCTTCATCCTCGAGGAGGGTGCCACTCTCCGCAACGTCATCATCGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     924 cgacggggcggatggtattcatctttacggtgatgccaaaatagacaatctgcacgtcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                864 ccagaaaccgctgtttatactggaagacggtgccagcctgaaaaacgtcaccatggggga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        726 GGATGTCTGCGAGGATGCCATCTCCATCCTTGGCAGCGGCACTGCCAAC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 143;
                                                              /organism="Fusarium solani f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50.2; DB Pred. No. 0.04;
                                                                                                                                                                         /gene="pelD"
join(348. .546,602. .1104)
/gene="pelD"
                                                                                                                                                                                                                                                                      /product-"pectate lyase D"
/protein_id-"AAC49420.1"
/db_xref-"GI:1526987"
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                                                                                                         /sub_species="pisi"
/db_xref="taxon:109625"
348. .1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            356
                                                                                                                                                                                                                                                                                                                                                                                                                                    DKSKGECEPSKAAKC
                                                                                     /isolate="T8"
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Best Local Similarity
Matches 161; Conserv
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                                               source
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ORIGIN
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                     FEATURES
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Υ.
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Fusarium solani f. sp. pisi

Eukaryota, Fundi; Ascomycota; mitosporic Ascomycota; Fusarium.

Eukaryota 1 to 1419)

Guo, W., Gonzalez-Candelas, L. and Kolattukudy, P.E.

Identification of a novel pelD gene expressed uniquely in planta by
Fusarium solani f. sp. pisi (Nectria haematococca, mating type VI)

and characterization of its protein product as an endo-pectate
                                                                                                         TATATAEPGVYTLRGHKWFTSAPWCDVFLVLAQAAGGLSCFLVPRVLPDGTRNTFRVQ
RLKDKLGNBSNASSEPEFDGTVAWLVGPEGGGVKTJIEWNUTRLDCVWASATLMRKT
LVACHHVRHRTAFGARLVDQPLMRNVLADLALESEAATATLRLAGAADRAVRGDEG
BAPRRIATAGKKVWVTKRGPAFTABALECLGGGVVEESGMPRHYRBAPLLSIWEGS
GNVNALDVLRALGRSAAAQALFGELSLARGABARLDAAADRLRTGITEASETGARRL
VELMALTLQASLLVRHAPPAVADAFCATRLGGDWGHAFGTLPDTADLDGILTRALPGE
                /translation="MTTLAQEPPYESYEPSEEPWGRPEGYATHDVTNQPPPLAPYDAS
DDYLLLEGIEREGAGWAEDGLARLGRAGSAQADWODLANREBPVETHDRYGNRYD
EVEYHPSWHHLMRVNYGEGLAGAPWADGRPGAHVARTAGGLVWGHTEAGHGCPTSMTY
AAVPALRAQPELAEVYEPLLTSREYEPGLRTPTDKRGLLAGMGMTEKQGGSDVRTNAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                               3690. .3782
/gene="2SCG38.05"
/note="Pfam match to entry PF00441 Acyl-CoA_dh, Acyl-CoA
dehydrogenase, score 2.10, E-value 8.7"
3981. .4778
                                                                                                                                                                                                                                                                                                                                                                                  /gene="2SCG38.05"
/note="Pfam match to entry PF00441 Acyl-CoA_dh, Acyl-CoA
dehydrogenase, score 224.20, E-value 5.9e-65"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSU13050 1419 bp DNA PLN 25-OCT-1999
Fusarium solani f. sp. pisi pectate lyase D (pelD) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2009 GCCGTCCTGAAGAACGTGATCATCGGCGCCCCGGCCGGCGGCGGCGTGCACTGCAAGGGC 2068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2183 GACGACAAGGTGTTCCAGTTCAACGGCGCGGAACGCTGAACATCTCCGGCTTCGCCGTC 2242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccaaacagcgcgggcaaaaatcccacgttgaaatcactaacagttccttcgagcacgcc 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tctgacaagatcctgcagctgaatgccgatactaacctgagcgttgacaacgtgaaggcc 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (05-AUG-1994) Wenjin Guo, Biotechnology Center, Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       835 gaattaggcgatggcggccagtctgaaaaccagaaaccgctgtttatactggaagacggt 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2069 AGTTGCACGCTCCAGAACGTCTGGTGGGAGGACGTCGGCGAGGACGCGGCGACCTTCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2129 GGCTCGTCGTCGTCGAACGTCTACACCG-----TCTCCGGCGGCGGCGCCAAGGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.6%; Score 61.4; DB 3; Length 40549;
51.4%; Pred. No. 5.1e-05;
Live 0; Mismatches 156; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arch. Biochem. Biophys. 332 (2), 305-312 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2243 AAGAACTICGGCACCTICGICCGGTCCTGCGGC 2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aaagactttggtactttgtacgcactaacggc 1167
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